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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 72512 Date: 10-19-05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 101072111
Location (Bldg/Room#): 2D22 (Mailbox #): 2018 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: TD & cloning of RET16

Inventors (please provide full names): C. G. Todd et al.

Earliest Priority Date: 2/15/02

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID Nos 12 & 13

- Nucleotide data bases only
- please include Interference

12 na 1272 Search

13aa 384

No size limits

6h-10/24/05

my

~~SECRET~~

Thanks.

STAFF USE ONLY

Searcher: Jan

Searcher Phone #: 22504

Searcher Location: _____

Date Searcher Picked Up: 10/24/05

Date Completed: 10/25/05

Searcher Prep & Review Time: 10

Online Time: 415

Type of Search

☒ NA Sequence (#)

☐ AA Sequence (#)

☐ Structure (#)

☐ Bibliographic

☐ Litigation

☐ Fulltext

☐ Other

Vendors and cost where applicable

☐ STN ☐ Dialog

☐ Questel/Orbit ☐ Lexis/Nexis

☐ Westlaw ☐ WWW/Internet

☒ In-house sequence systems

☒ Commercial ☐ Oligomer ☐ Score/Length
☒ Interference ☐ SPDI ☒ Encode/Transl
☐ Other (specify)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM proteoin - nucleic search, using frame_plus_p2n model

Run on: October 24, 2005, 16:20:38 ; Search time 480 Seconds
(without alignments)
4735.793 million cell updates/sec

Title: US-10-077-111-13

Perfect score: 2047
Sequence: 1 MVKLITLADHGDVNCACF.....LTPNRLKMAINRWLETHQK 384

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=x1h
-Q=/cg12_1/USPTO.epool/US10077111/runat_24102005_072845_8155/app.query.fasta.1.553
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdt
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N-Geneseg_16Dec04.*

1: geneseqn1980s:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2047	100.0	1272	6	AAD45075 Human RET
2	1984	96.9	1553	6	AAD45071 Human RET
3	1984	96.9	1818	6	AAD45070 Human RET
4	1984	96.9	1996	5	ABV25028 Human pro
5	1984	96.9	1996	5	ABV23190 Human pro

6	1978	96.6	1773	8	AB224707	AB224707 Human cel
7	1978	96.6	1811	10	ADB63535	ADB63535 Human CDN
8	1978	96.6	1817	10	ADB47507	ADB47507 Human CDN
9	1978	96.6	1844	4	AA158876	AA158876 Human pol
10	1978	96.6	1844	5	AAD99098	AAD99098 DNA encod
11	1978	96.6	1844	9	ADB48858	ADB48858 Novel hum
12	1958	95.7	1908	6	AAD45076	AAD45076 Human RET
13	1854	90.6	1633	4	AA164914	AA164914 Beta-cran
14	1853.5	90.5	1826	5	AA160662	AA160662 Human pol
15	1715.5	83.8	1686	5	ADM19385	ADM19385 Novel hum
16	1616.5	79.0	1901	6	AAD45073	AAD45073 Mouse RET
17	1226.5	59.9	1291	4	AAF58364	AAF58364 Human GTP
18	1000	48.9	838	5	ADM19628	ADM19628 Novel hum
19	717.5	35.1	668	13	ADQ54461	ADQ54461 Novel can
20	709	34.6	630	6	AAD45072	AAD45072 Human RET
21	627.5	30.7	446	5	ABV05038	ABV05038 Human pro
22	626.5	30.6	409	5	ABV14207	ABV14207 Human pro
23	621.5	30.4	441	5	ABV35301	ABV35301 Human pro
24	621.5	30.4	441	5	ABV44135	ABV44135 Human pro
25	597	29.2	366	4	AA136816	AA136816 Probe #55
26	597	29.2	366	4	AAK30903	AAK30903 Human bon
27	597	29.2	366	4	AAK05311	AAK05311 Human bra
28	597	29.2	366	4	ABK30581	ABK30581 Human liv
29	597	29.2	366	6	ABK05651	ABK05651 Human gen
30	532	26.0	297	4	AA150015	AA150015 Probe #18
31	532	26.0	297	4	AAK44005	AAK44005 Human bon
32	532	26.0	297	4	AAK18116	AAK18116 Human bra
33	532	26.0	297	4	ABK34659	ABK34659 Human liv
34	532	26.0	297	6	ABK18238	ABK18238 Human gen
35	509	24.9	419	3	AAH30188	AAH30188 Human col
36	352	17.2	520	6	AAD45074	AAD45074 Rat RET16
37	318	15.5	399	5	AAF66462	AAF66462 Novel hum
38	308.5	15.1	466	4	ABK58107	ABK58107 Human foe
39	308.5	15.1	466	4	AA137710	AA137710 Probe #63
40	308.5	15.1	466	4	AAK31840	AAK31840 Human bon
41	308.5	15.1	466	4	AAK06182	AAK06182 Human bra
42	308.5	15.1	466	4	ABK31528	ABK31528 Human liv
43	308.5	15.1	466	6	ABK06599	ABK06599 Human gen
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45	300	14.7	180	4	AA150879	AA150879 Probe #19

ALIGNMENTS

RESULT: 1	
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ID	AAD45075 standard; DNA; 1272 BP.
AC	AAD45075;
XX	
DT	27-DEC-2002 (first entry)
XX	
DE	Human RET16.2 splice variant DNA.
XX	
KW	Human; RET16; intracellular signal; inflammation-related disease; aschma;
KW	rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotection;
KW	transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
KW	infective respiratory bowel disease; Crohn's disease; immunosuppressive; cancer;
KW	autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
KW	cellular migration disorder; cell proliferation disorder; calcification;
KW	hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
KW	cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
KW	thalassaemia; vasotropic; gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	
FT	Key
FT	CDS
XX	Location/Qualifiers
FT	111..1265
FT	/tag= a
FT	/product= "Human RET16.2 splice variant protein"
XX	
PN	WO20026494-A2.

XX 29-AUG-2002.
 PD
 XX
 PF 15-FEB-2002; 2002MO-US005162.
 XX
 PR 16-FEB-2001; 2001US-0269366P.
 XX PR 29-MAY-2001; 2001US-0294181P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Todderud CG, Finger JN, Rillema J;
 XX MPI; 2002-682760/73.
 DR P-PSDB; AAE28167.
 XX
 PT New human, mouse or rat RET16 genes and proteins, involved in
 PT intracellular signaling cascade, useful for in gene therapy, particularly
 PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
 PT tumors or neoplasms.
 XX
 XX Claim 1; Page 166; 175pp; English.
 CC The invention relates to human, mouse or rat RET16 genes and proteins,
 CC involved in intracellular signaling cascade. The RET16 protein or
 CC polynucleotide is useful for treating an inflammation-related disease or
 CC disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
 CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
 CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
 CC bowel disease, Crohn's disease, ulcerative colitis, inacute respiratory
 CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
 CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
 CC disease or disorder also includes disorders associated with aberrant
 CC activation of the TNF-alpha pathway, disorders associated with aberrant
 CC cellular migration, proliferation, metastasis, juvenile idiopathic
 CC arthritis, haematogenous metastases of tumour cells, hyperinsulinaemia,
 CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
 CC tumour progression, Wegener's granulomatosis, stem cell transplantation
 CC complications, ischaemia-reperfusion injury, thalassemia, acute lung
 CC injury, graft rejection, ischaemic heart, coronary artery calcification
 CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
 CC sequence is human RET16.2 splice variant DNA
 XX
 XX Sequence 1272 BP; 349 A; 269 C; 290 G; 364 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1,33e-191 Length: 1272
 Score: 2047.00 Matches: 384
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-077-111-13 (1-384) x AAD45075 (1-1272)
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 Db 111 ATGCTGAACCTGATTCACATTAAGTCGATCGATGTCAGATGCAACTGCTGCTTC 170
 QY 21 SerPheSerLeuLeuAlaThrCybSerLeuAspLyThrIleArgLeuTySerLeuArg 40
 Db 171 TCCCTTTCCCTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
 QY 41 AspPheThrGluLeuProHisSerProLeuLybPheHisThrTyAlaValHisCybCyb 60
 Db 231 GACTTTACTAATCTGCACATTCCTCCATGAAGTTTATACCTATGCTGCTGCTGCTGCTG 290
 QY 61 CybPheSerProSerGlyHisIleLeuAlaSerCybSerThraSpGlyThrThrValLeu 80
 Db 291 TGTTTCTCCCTCCAGACATATTGTCATCGGTCGTTCAACAAGTGTATACACATGCTCTA 350
 QY 81 ThrAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
 Db 351 TGGAAATACTGAAATGACAGATGCTGGCAGTGTGAAACAGCCTAGTGGCAGCCCTGTG 410

QY 101 ArgValCybGlnPheSerProAspSerThrCybLeuAlaSerGlyValAlaAspGlyThr 120
 Db 411 AGGGTTTGCACAGTTTCCCCACAGCTCCAGCTGTTGGCATTCAGGGGACCTATGGAAC 470
 QY 121 ValValLeuThrAsnAlaGlnSerTybLeuTyArgCybGlySerValLybAspGly 140
 Db 471 GTGGTTTGTGGAAATGACAGTCATCAAAATTAATAGATGTGTGTGTAAAGATGCG 530
 QY 141 SerLeuAlaAlaCybAlaPheSerProAsnGlySerPhePhoValThrLybSerCyb 160
 Db 531 TCCCTGGCGGCAATGTCATTTCTCTAAATGAAGCTTTTGTCACTGCTCTCATGT 590
 QY 161 GlyAspLeuThrValThrPheAspLybMetArgCybLeuHisSerGlybAsp 180
 Db 591 GGTGATTTAACTGCTGCGATGATATAAAATGAGTGCTGTCTCATAGTAAAGACACATGAT 650
 QY 181 LeuGlyIleThrCybCybAspPheSerSerGlnProValSerAspGlyGlnGlyLeu 200
 Db 651 CTGGAATTAACCTGCTGCGATTTTCTTCACAGCCAGTTTGTATGACAGAACAGGCTCT 710
 QY 201 GlnPhePheArgLeuAlaSerCybGlyGlnAspCybGlnValLybIleThrPheValSer 220
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 QY 221 PheThrHisIleLeuAlaArgArgThrGluHisGlnLeuLybGlnPheThrGluAspThr 240
 Db 771 TTTTACCATTCCTTACCAAGCGGCACAGAACATCAGCTGACCAACATTTTCCGAAAGTTG 830
 QY 241 SerGluGluValaValSerThrThrPheCybAlaGlnAspLeuLybAspLeuValGlyIle 260
 Db 831 TCAGAGAGAGTGTCTCAACATGCGCTTGTGCACAAAGATTTTAAAGATCTTGTGTATT 890
 QY 261 PheLybMetAspAsnIleAspGlyLybGluLeuLeuAspLeuThrLybGluSerLeuAla 280
 Db 891 TTCAAATGAATAACCTTATATGAAAGAACTGTGAATCTTACAAAGAAAGTCTGGCT 950
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 QY 301 LeuArgThrLybValaLybSerLeuSerSerGlyIleProAspGluPheIleCysProIle 320
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 Db 1071 ACTAGAAACCTTATGAAAGATCCGGTCATCGCATCAGATGGCTATTCAATGAAAGAA 1130
 QY 341 AlaMetGluAsnThrIleSerLybLybAspArgThrSerProMetThrAsnLeuValLeu 360
 Db 1131 GCATGGAATAATGATGATCAGCAAAAAGAAACGACAAAGTCCCATGCAATCTGTGTTCT 1190
 QY 361 ProSerAlaValLeuThrProAsnArgThrLeuLybMetAlaIleAsnArgThrPheGlu 380
 Db 1191 CTTTACAGCGGCTTACTTACCAAAATAGAGCTTGAATAATGCCATCAATGATGCTGAGAG 1250
 QY 381 ThrHisGlnLyb 384
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 RESULT 2
 AAD45071
 ID AAD45071 standard; DNA: 1553 BP.
 XX
 AC AAD45071;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human RET16 open reading frame (ORF) DNA.
 XX
 KW Human; RET16; intracellular signal; inflammation-related disease; asthma;
 KW rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;

KM transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
 KM inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
 KM inacute respiratory distress syndrome; cardiast; ulcerative colitis;
 KM autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
 KM cellular migration disorder; cell proliferation disorder; calcification;
 KM hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
 KM cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
 KM thalassemia; vasotropic; open reading frame; ORF; gene; ds.
 OS Homo sapiens.
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 XX Key Location/Qualifiers
 FH CDS 3..1541
 FT /*tag= a
 FT /product= "Human RET16 protein"
 FT /note= "CDS does not include start codon"
 FT /partial
 XX WO20026494-A2.
 XX
 XX 29-AUG-2002.
 XX
 XX 15-FEB-2002; 2002WO-US005162.
 XX
 XX 16-FEB-2001; 2001US-0269366P.
 XX 29-MAY-2001; 2001US-0294181P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Todderud CG, Finger JN, Rillema J;
 PI
 XX WPI: 2002-682760/73.
 DR P-PSDB; AAE28164.
 DR
 PT New human, mouse or rat RET16 genes and proteins, involved in
 PT intracellular signaling cascade, useful for in gene therapy, particularly
 PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
 PT tumors or neoplasms.
 PS
 PS Claim 1; Page 150; 175pp; English.
 XX
 XX The invention relates to human, mouse or rat RET16 genes and proteins,
 CC involved in intracellular signaling cascade. The RET16 protein or
 CC polynucleotide is useful for treating an inflammation-related disease or
 CC disorder, e.g. rheumatoid arthritis; juvenile arthritis; psoriasis,
 CC asthma, ischemia-reperfusion, multiple sclerosis, rejection of organ or
 CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
 CC bowel disease, Crohn's disease, ulcerative colitis, inacute respiratory
 CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
 CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
 CC disease or disorder also includes disorders associated with aberrant
 CC activation of the TNF-alpha pathway, disorders associated with aberrant
 CC cellular migration, proliferation, metastasis, juvenile idiopathic
 CC arthritis, haemogenous metastases of tumour cells, hyperinsulinaemia,
 CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
 CC tumour progression, Wegener's granulomatosis, stem cell transplantation
 CC complications, ischaemia-reperfusion injury, thalassemia, acute lung
 CC injury, graft rejection, ischemic heart, coronary artery calcification
 CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
 CC sequence is human RET16 open reading frame (ORF) DNA
 XX
 SO Sequence 1553 BP; 428 A; 327 C; 348 G; 450 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.86e-185 Length: 1553
 Score: 1984.00 Matches: 383
 Percent Similarity: 80.46% Conservative: 0
 Best Local Similarity: 80.46% Mismatches: 1
 Query Match: 96.92% Indels: 92
 DB: Gaps: 1

US-10-077-111-13 (1-384) x AAD45071 (1-1553)

Qy 1 MetValIysLeuIleHisThrIleuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
 Db 111 ATGCTGAACACTGATTACACATTAGCTGATCAGGACAGATCTCACTGCTTCT 170
 Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
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 Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
 Db 231 GACTTTACTGAACTGCACATTTCTCCATTCGAACTTCAATCACTTATGCTGCTGCTG 290
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 Qy 121 ValValLeuThrPheAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
 Db 471 GTGGTTTGTGGAATGACAGCTCATCAAAATTATATGATGTGACTGTTAAAGATGCG 530
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 Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlyLeu 200
 Db 651 CTGGAAATTAACCTGCTGCGATTTTCTTTCACAGCCAGTTTCTGATGGAACAAAGCTTT 710
 Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTyrIleValSer 220
 Db 711 CAGTTTGTGACATGGCATCATGGTACAGATTTGCCAAATGAAATTTGGATTTGTTCT 770
 Qy 221 PheThrHisIleLeu----- 225
 Db 771 TTTAACCAATATCTTAGGTTTGAATTAAATATTAAGTAACTGAGTGGGCACTGTGCT 830
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 Qy 225 ----- 225
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 Db 1131 CTTTGTGCACAAATTTAAAGATCTTGTGTGATTTTCAAGATGATTAACATTGATGAGA 1190
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Db 1251 GGGCTGCGAGTAAATGCTGGAGAAAATTGGAAGCTCGAGCAAGGTTAAATCCCTT 1310
Qy 309 SerSerGlyLeuProAArgPheLeuCyPProGleThraArgLileuMetVleAArgPro 328
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Qy 329 ValIleAlaSerAArgPlyThrySerThryGluVleGluAlaMetGluAArgPlySerLeu 348
Db 1371 GTCATCGCATCAAGATGGCTATTCATATGAAAAGAAAGCAATGAAAATTGATCAGCAA 1430
Qy 349 VleGlyAArgThrySerProMetThraArgLeuValLeuProSerAlaValLeuThraArg 368
Db 1431 AAGAAACGTAACAGTCCATGACAAATCTTCTTCCTTCACGCGGTACTTACACCAAA 1490
Qy 369 ArgThryLeuMetAlaIleAArgThryPleuGluThryHisGlnVle 384
Db 1491 AGGACTCTGAAAAATGGCCATCATAGATGGCTGAGACACACCAAAAG 1538

RESULT 3
AAD45070
ID AAD45070 standard; DNA; 1818 BP.
AC AAD45070;
DT 27-DEC-2002 (first entry)
DE Human RET16 DNA.
XX
XX Human; RET16; intracellular signal; inflammation-related disease; asthma;
XX rheumatoid arthritis; psoriasis; multiple sclerosis; neuroproective;
XX transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
XX inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
XX inactive respiratory distress syndrome; cardiac; ulcerative colitis;
XX autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasia;
XX cellular migration disorder; cell proliferation disorder; calcification;
XX hyperinflammation; diabetes type 2; systemic lupus erythematosus; tumour;
XX cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
XX thalassemia; vasotropic; gene; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 148..1578
XX FT /tag= a
XX FT /product= "Human RET16 protein"
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XX MO200266494-A2.
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XX PD 29-AUG-2002.
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XX PP 15-FEB-2002; 2002MO-US005162.
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XX PR 16-FEB-2001; 2001US-0269366P.
XX PR 29-MAY-2001; 2001US-0294181P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Todderud CG, Finger JN, Rillema J,
XX PI
XX DR MPI, 2002-682760/73.
XX DR P-PSDB; AAB28163.
XX
XX New human, mouse or rat RET16 genes and proteins, involved in
XX intracellular signaling cascade, useful for in gene therapy, particularly
XX for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
XX tumors or neoplasia.
XX
XX Claim 1; Page 147-148; 175pp; English.
```

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XX
CC The invention relates to human, mouse or rat RET16 genes and proteins,
CC involved in intracellular signaling cascade. The RET16 protein or
CC polynucleotide is useful for treating an inflammation-related disease or
CC disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
CC bowel disease, Crohn's disease, ulcerative colitis, inactive respiratory
CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
CC cystic fibrosis, cancers, tumours or neoplasias. This inflammation-related
CC disease or disorder also includes disorders associated with aberrant
CC activation of the TNF-alpha pathway, disorders associated with aberrant
CC cellular migration, proliferation, metastasis, juvenile idiopathic
CC arthritis, haematogenous metastases of tumour cells, hyperinflammation,
CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
CC tumour progression, Wegener's granulomatosis, stem cell transplantation
CC complications, ischaemia-reperfusion injury, thalassemia, acute lung
CC injury, graft rejection, ischaemic heart, coronary artery calcification
CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
CC sequence is human RET16 DNA.
XX
XX
XX Sequence 1818 BP; 523 A; 373 C; 382 G; 540 T; 0 U; 0 Other:
```

```
Alignment Scores:
Pred. No.: 3,58e-185 Length: 1818
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 6 Gaps: 1
```

US-10-077-111-13 (1-384) x AAD45070 (1-1818)

```
Qy 1 MetValVleLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnProGlyAlaPhe 20
Db 148 ATGGTAAACGTATTCACATTAGCTGATCAAGGAGATGTCACATCGTGGCTTC 207
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAArgPlyThrIleArgLeuThrySerLeuAArg 40
Db 208 TCTTTTCCCTCTGGCTACTGCTCTCTTGACAAACAATTCGCTGATCTGTTACGT 267
Qy 41 AspPheThrGluLeuProHisSerProLeuVlePheHisThrThyAlaValHisCysCys 60
Db 268 GACTTACTGAACCTGGCCATCTTCATGAAATTCATACCGATGCTGCACTCTG 327
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu 80
Db 328 TGTTCCTCCCTTCAGGACATATTTGGCATGCTGTCAACAGATGTACCACTGTCTTA 387
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 388 TGGAAATACGAAATATGACAGATGCTGGCAGTGAAGAAACAGCTTATGTCAGCCCTG 447
Qy 101 ArgValCysGlnPheSerProAArgPheThryCysLeuAlaSerGlyAlaAlaArgPlyThr 120
Db 448 AGGGTTTGGCAGTTTCCCAAGCTCCACGTTGGTCATCGGGCCACCTGATGMACT 507
Qy 121 ValValLeuThrAsnAlaGlnSerThryVleThryArgCysGlySerValVleAspGly 140
Db 508 GTGGTTTGTGGATGACAGATCATACAAATTAATTAAGTGTGATTAAGATGGC 567
Qy 141 SerLeuAlaAlaCysValaPheSerProAArgPheThryCysLeuAlaSerGlySerCys 160
Db 568 TCTTGGCGGATGTCATTTCTCTTAATGAAAGCTTTTGTGCACTGGCTCTGATG 627
Qy 161 GlyAspLeuThrValTrpAsnArgPlyMetArgCysVleHisSerGlyValAlaHisAsp 180
Db 628 GGGATTTTAAACAGTGGCATGATGATAAATGAGGTGCTCATATGTAAGAAACACATGAT 687
Qy 181 LeuGlyIleThrCysGlyAspPheSerSerGlnProValSerAspGlyValGluGlnGlyLeu 200
Db 688 CTTGGAATTAACCTGTCGATTTTCTTTCACAGCCAGTTTGTGATGGAACAAAGGTCTT 747
```

QY 201 GlnPhePheargLeuAlaSerCysGlyGlnAspCysGlnValIleThrPileValSer 220
DB 748 CAGTTTTCGACATGCGATCATGTGGTCAGAGATTGCCAACTCAAAATTGGATTGTTCT 807
QY 221 PheThrHisIleLeu----- 225
DB 808 TTTACCAATATCTTAGTATTAAATATATAAGTACACAGTGGGCACTGTGT 867
QY 225 ----- 225
DB 868 CCGTTCTGGCTTGTCTTTTCCCATGATGAGGAGATGCTACTCAGGGTCAGTGAT 927
QY 225 ----- 225
DB 928 AACTGTGCTATGATATATGATTAATACTGAGAAATATCTTCACACATGACTCAGCAC 987
QY 225 ----- 225
DB 988 ACCAGTATGTCAACAATTGTGCTTTGACACTAATACCCTTTACTTGTGCTACTGTTCA 1047
QY 226 -----AlaArgArg 228
DB 1048 ATGACAAACAACTGAAACATCTGCGCAATTGACCTGGAAACACTTGGCCAAAGAGCGC 1107
QY 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTrp 248
DB 1108 ACGAAACATAGCTGAGCAATTTACCGAAGATTGGTCAGAGGAGATGCTCAACATGG 1167
QY 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
DB 1168 CTTTGTGACACAGATTTAAAGATCTGTGTGATTTTCAAGATGATTAACATTGATGGA 1227
QY 269 LysGluLeuLeuLeuLeuLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
DB 1228 AAGAACTGTGATCTTACAAAGAAAGTCTGCTCATATTTGAAATTTGAAATCTCTA 1287
QY 289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
DB 1288 GGACTGCTGTAAGTAAAGTCTGAGGAAATTTGAGAGCTCAGACCAAGGTTAAATCCCTT 1347
QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
DB 1348 TCTTCAGAGAAATCTGATGATTAATATATGTCCAATACTAGAGAACTTATGAAAGATCCG 1407
QY 329 ValIleAlaSerAspGlyTrpSerTrpGluLysGluAlaMetGluLeuThrPileSerLys 348
DB 1408 GTCATGCAATCAGATGCTATCTATGAAAGAGAACCAATGGAATTTGGATCAGCAAA 1467
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1468 AAGAAACGTACAGTCCCATGACAAATCTGTTCTTCTCAGCGGTACTTACACCAAT 1527
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
DB 1528 AGAAGCTCTGAATAATGGCCATCAATAGATGGCTGAGACACACCAAAAG 1575
RESULT 4
ABV29028 ID ABV29028 standard; cDNA; 1996 BP.
AC ABV29028;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 29019.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX MO200160860-A2.

PD 23-AUG-2001.
XX
XX 20-FEB-2001; 2001MO-US005171.
XX
XX 17-FEB-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1, Page 6145-6146; 11750pp; English.
PS
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1996 BP; 615 A; 378 C; 447 G; 543 T; 0 U; 13 Other;
XX
Alignment Scores:
Pred. No.: 4.09e-185 Length: 1996
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: Gaps: 1
US-10-077-111-13 (1-384) x ABV29028 (1-1996)
QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
DB 16 ATGGTGAACTGATTCACACATTAGCTGATCAATGACATGTCNACTGCTGCTTC 75
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTrpSerLeuArg 40
DB 76 TCCCTTTCCTCTTGGTACTTCTGCTCCTTGACAAACAAATTCGCTGATCTGTTACGT 135
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTrpAlaValHisCysCys 60
DB 136 GACTTTACTAATCTGCACATCTCTCAATGAAATTCATACCTATGCTGTCACCTGTC 195
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB 196 TGTTTCTCCCTTCAGGACATATTTTGGCATGCTGTTCAACAGATGTTACACATGCTCTA 255
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
DB 256 TGGAAATCTGAAATAGACAGATGCTGAGTATGAGAAACAGCTTGTGCGACGCTGTG 315
QY 101 ArgValCysGlnInPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
DB 316 AGGGTTTGGCAGATTTTCCCGAGCTCCACGTGTTTGGCATCAGGGGCGAGCTGATGAACT 375
QY 121 ValValLeuThrPheAlaGlnSerTrpLysLeuTrpArgCysGlySerValLysAspGly 140

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Db 376 GTGGTTTGTGGAAATGCACAGTCATCAAAATTATATAGATGTGTGTTAAAGATGGC 435
Qy 141 SerLeuAlaAlaCyAlaPheSerProanGlySerPhePheValThrGlySerSerCyS 160
Db 436 TCCCTGGCGGCGATGTCATTTTCTCTTAATGGAAGCTTCTTGTCACTGGCTCCTCATG 495
Qy 161 GlyAapLeuThrValTrrPaapAapLysMetArgCysLeuHisSerGlyLysAlaHisAap 180
Db 496 GGTGATTTTAACACTGTGGGATGATTAATAAGAGTGTCTGATAGTGAATAAGACATGAT 555
Qy 181 LeuGlyIleThrCysCysAapPheSerSerGlnProValSerAapGlyLugInGlyLeu 200
Db 556 CTGGGAATTACCTGCTGCCATTTTCTTCTCAACAGCTTCTGATGAGAAACAAGTCTT 615
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAapCysGlnValIleThrPileValSer 220
Db 616 CAGTTTTCGACTGGCATCATGTGTGTCAGAGATTGGCCAAGTCAAAATTTGGATTGTTCT 675
Qy 221 PheThrHisIleLeu----- 225
Db 676 TTTTACCATATCTTTAGCTTTTGAATTAATAATATAAAAGTACACTGAGTGGCACTGTCT 735
Qy 225 ----- 225
Db 736 CCGTTCTGGCTTGCTGCTTTTCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGAT 795
Qy 225 ----- 225
Db 796 AAGTCTGTATAGTATATGATACTAATACTAGAGAATAATACCTGACACTGACTCAGAC 855
Qy 225 ----- 225
Db 856 ACCAGGATGTCAACAATTGTGCTTTTGCACTTAATACCTTTACTTGCTACTGCTCA 915
Qy 226 -----AlaArg 228
Db 916 ATGACAAAACAGTGAACATCTGCAATTGACCTGAAAACACTTTGCCAAGCAAGCGCG 975
Qy 229 ThrGlnHisGlnLeuLysGlnPheThrGlnAapTrpSerGlnLysValValIleSerTrp 248
Db 976 ACAGAACATCAGCTGAAGCAATTTACCGAAGATTGGTCAGAGAGAGATGTCCTCAACATGG 1035
Qy 249 LeuCyAlaGlnAapLeuLysAapLeuValGlyIlePheLysMetAsnAniLeaPgly 268
Db 1036 CTTTGGCACACAGATTTTAAAGATCTTGTGGTATTTTCAAGTGAATTAACATTGATGCA 1095
Qy 269 LysGlnLeuLeuAanLeuThrLysGlnSerLeuAlaAapAapLeuLysIleGlnSerLeu 288
Db 1096 AAGAAGCTGTGAATCTTACAAAAGAAAGCTGGCTGATGATTTGAAAATTGAATCTCTA 1155
Qy 289 GlyLeuAapSerLysValLeuAapGlyLysIleGlnGlnLeuArgThrLysValLysSerLeu 308
Db 1156 GGACTCGTAGTAAAGTGTGAGGAAAATTGAAGAGCTCAGACCAAGGTAAATCCCTT 1215
Qy 309 SerSerGlyIleProAapGlnPheIleCysProIleThrArgLysLeuMetLysAapPro 328
Db 1216 TCTTCAGAAATTCCTGATGATTAATGATTCGCAATTAACCTTAAGAAAGATCCG 1275
Qy 329 ValIleAlaSerAapGlyLysSerLysGlnLysGlnAlaMetGlnAanTrpIleSerLys 348
Db 1276 GTCATCGCATCAGATGCTATTCATATGAAAAGAAAGCAATGAAAATTGATCAGACAAA 1335
Qy 349 LysLysArgThrSerProMetThrAanLeuValLeuProSerAlaValLeuThrProAn 368
Db 1336 AAGAAAAGTACAGATCCCATGACAAATCTTGTCTTCACGCGGTACTTACACCAAAAT 1395
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHisGlnLys 384
Db 1396 AGGACTCTGAATAATGGCCATCATAGATGCTGGAAGACACACCAAAAG 1443
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ID ABV23190 standard; cDNA; 1996 BP.
XX
AC ABV23190;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 23181.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; 88.
XX
OS Homo sapiens.
XX
PN MO200160860-A2.
XX
PD 23-ANG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-018319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-021314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 4166-4167; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (i) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement; (i) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1996 BP; 615 A; 378 C; 447 G; 543 T; 0 U; 13 Other;
XX
Alignment Scores:
Pred. No.: 4, 09e-185 Length: 1996
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Beer Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 5 Gaps: 1
US-10-077-111-13 (1-384) x ABV23190 (1-1996)
Qy 1 MetValLysLeuIleHisThrLeuAlaAapHisGlyAapAapValAnncysCyAlaAap 20
Db 16 ATGGGAAACGTAGTTTCAACATTAAGCTGATGAGAGAGTCAATGCTGTGCTTTC 74
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAapLysThrIleArgLeuLysSerLeuArg 40
Db 76 TCCCTTTCCTCTGCTGCTAGCTTGCCTTGGACAAACAAATTCGCTGATCTGTTACGT 135
Qy 41 AspPheThrGlnLeuProHisSerProLysLysPheHisThrTyraAlaValHisCysCyS 60
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RESULT 5
ABV23190
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Db      136 GACTTACTGAACTGCACATTCCTCATGTGAAGTTTCATACCTATGCTGCTCACTGCTGC 195
Qy      61 CyepheserProsergylhisileleuAlaserCyserThrapgilyThrValleu 80
Db      196 TGTTCCTCCCTTCAGACATATTTTGGCATCGGTTCACAGATGGTACACACTGCTCTA 255
Qy      81 TrpAsnThrGluanglygImetleuAlaValmetGluInProsergylSerProVal 100
Db      256 TGGAAATCTGAAAAATGACAGATCTCTGGCATGTGAAACAGCTTAGTGAGCCCTGTG 315
Qy      101 ArgValCysGlnPheSerProAspSerThrCysleuAlaserGlyAlaAlaaspGlyThr 120
Db      316 AGGATTGGCCAGTTTCCCGACACTCCAGCTGTGGCATCAGGGGCGCTGATGGAAC 375
Qy      121 ValValleuThrPheAsnAlaGlnSerTyrLysleuTyrArgCysGlySerValLysaspGly 140
Db      376 GTGGTTTTGGGAATGACAGATCATACAAATTAATATGATGTGATGTTAAAGATGCG 435
Qy      141 SerleuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db      436 TCCTTGGCGGCGATGTCATTTTCTCTTAATGGAAGCTTCTTGTCACTGGCTCCTCATGT 495
Qy      161 GlyAspleuThrValTTPAspAspLysPheArgCysleuHisSerGlyLysAlaHisAsp 180
Db      496 GGTGATTTAAACAGTGTGGATGATAAATAGTGTCTGTCATAGTGAAGAAAGCACATGAT 555
Qy      181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db      556 CTGGGAATTCCTGCTCGATTTTCTTTCACAGCAGATTTCTGATGAGAACAAAGGCTT 615
Qy      201 GlnPhePheArgleuAlaSerCysGlyGlnAspCysGlnValLysIleTPIleValSer 220
Db      616 CAGTTTTTGCAGCTGGCATCATGTGTCAGGATGCCAAGTCAAAATTTGGATTTGTTCT 675
Qy      221 PheThrHisIleLeu----- 225
Db      676 TTTACCATATCTTAGGTTTGAATTAATAATAAAGTACACAGTGGGCACTGTGCT 735
Qy      225 ----- 225
Db      736 CTTGTTCTGGCTTGCTTTTCCCATGATGGGAGATGCTAGTCTCAGGGTCACTGGAT 795
Qy      225 ----- 225
Db      796 AAGTCTGTCAATATGATATCTAATACTGAGATATCTTCAACACTTGACTCAGCAC 855
Qy      225 ----- 225
Db      856 ACCAGTATGTCACACACTGTGCTTTGGACCTAATACCTTTTACTTGCTACTGTTCA 915
Qy      226 -----AlaArgArg 228
Db      916 ATGACAAAAACAGTGAACATCTGGCAATTGGACCTGGAACACTTTGCCAAGCAGGCGC 975
Qy      229 ThrGluHisGlnleuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTyr 248
Db      976 ACAGAACATCACTGAGACCAATTTTACCGAAGATTTGGTCAGGAGATGTCTCAACATGG 1035
Qy      249 LeuCysAlaGlnAspleuLysAspleuValGlyIlePheLysMetAsnAlaaspGly 268
Db      1036 CTTTGTGCACAAAGTTTAAAAAGATCTTGTTGATTTTTCAGAAAGATTAACATTGATGGA 1095
Qy      269 LysGluLeuLeuAsnleuThrLysGluSerleuAlaAspAspleuLysIleGluSerleu 288
Db      1096 AAAGAACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAAATGGAATCTCTA 1155
Qy      289 GlyLeuArgSerLysValIleuArgLysIleGluGluLeuArgThrLysValLysSerleu 308
Db      1156 GGACTGCTGTAATAAGTGTGAGGAAATGAAAGGCTCAGACACAAAGTTTAAATCCCTT 1215
Qy      309 SerSerGlyIleProaspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db      1216 TCTTCAGGAATTCCTGATGATATTAATATGTCATTAAGTAAGAACTTATGAAAGATCCG 1275

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Qy      329 ValIleAlaSerAspGlyTyrSerTyrGluLysGluAlaMetGluAsnTrpIleSerLys 348
Db      1276 GTCATGTCATCAATGAGTCTATCATATGAAGAACCAATGAAATTTGATCAGCAA 1335
Qy      349 LysLysArgThrSerProMetThrAsnLeuValleuProSerAlaValIleThrProAsn 368
Db      1336 AAGAAAGCTAACAGTCCCAAGACAAATCTTGTCTTCTTCAAGCGGATCTTACACCAAT 1395
Qy      369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
Db      1396 AGGACTCTGAAAATGCGCATCAATAGATGCTGGAGACACACAAAG 1443

RESULT 6
ABZ24707
ID      ABZ24707 standard; cDNA; 1773 BP.
XX
AC      ABZ24707;
XX
DT      07-APR-2003 (first entry)
XX
DE      Human cell growth, differentiation and death protein CGDD-19 cDNA.
XX
KW      CGDD-19; cell growth; cell differentiation; cell death; human;
KW      cytosolic; antiarteriosclerotic; hepatotropic; antiinflammatory;
KW      antiparasitic; antianemic; ophthalmological; auditory; antiviral;
KW      cerebroprotective; nootropic; neuroprotective; antiParkinsonian;
KW      neuroleptic; tranquilizer; immunosuppressive; anti-HIV; antiallergic;
KW      antiaesthetic; antithyroid; antidiabetic; dermatological; nephrotropic;
KW      antineumatic; antiarthritic; anticancer; vulnary; virucide;
KW      antibacterial; fungicide; antiparasitic; protozoicide; antihelminthic;
KW      antifertility; gynaecological; gene therapy; microarray; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      60..1490
FT      /*tag= a
FT      /product= "Human CGDD-19"

W0200297032-A2.
PD
XX      05-DEC-2002.
XX
PF      05-APR-2002; 2002W0-US011152.
XX
PR      06-APR-2001; 2001US-0282110P.
PR      11-APR-2001; 2001US-0283294P.
PR      26-APR-2001; 2001US-0286820P.
PR      27-APR-2001; 2001US-0287228P.
PR      16-MAY-2001; 2001US-0291662P.
PR      18-MAY-2001; 2001US-0291846P.
PR      25-MAY-2001; 2001US-0293727P.
PR      01-JUN-2001; 2001US-0295263P.
PR      01-JUN-2001; 2001US-0295340P.
PR      15-JAN-2002; 2002US-0349705P.
XX
XX      (INCY-) INCYTE GENOMICS INC.
XX
PI      Azimzai Y, Au-Young JK, Batra S, Baughn MR, Becha SD;
PI      Borowkai ML, Burford N, Ding L, Elliott VS, Emerling BM, Gandhi AR;
PI      Gietzen KJ, Griffin JA, Hafalia AJA, Honchell CD, Lal PG, Lee SY;
PI      Lu DM, Arvizu GS, Ramkumar J, Reddy R, Sanjanwala MM, Tang YT;
PI      Walia NK, Wang YE, Warren BA, Xu Y, Yang J, Yao MG, Yue H;
PI      Zebajadian Y;
XX
XX      WPI: 2003-140453/13.
XX      P-PSDB: ABP58348.
XX
PT      Novel human proteins associated with cell growth, differentiation and
PT      death, useful for treating, diagnosing or preventing cancer,
PT      developmental, neurological, reproductive or autoimmune/inflammatory
PT      disorders.

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XX Claim 5: Page 235-236; 238bp; English.

CC The present sequence is that of Incyte clone 7483131CBI encoding human
CC CGDP-19, a novel protein associated with cell growth, differentiation and
CC death. A representative cDNA library for the polynucleotide is KIDN0T19
CC derived from kidney tissue. Structural features establish the encoded
CC protein as being associated with cell growth, differentiation and death,
CC and as showing sequence and structural similarity to human apoptotic
CC protease activating factor 1. The invention is based on novel human CGDP-
CC 1 to -21 proteins (see ABP58330-50), the polynucleotides encoding them
CC (see ABP24689-709), and to the use of these for the diagnosis, treatment
CC or prevention of cell proliferative disorders including cancer,
CC developmental disorders, neurological disorders, autoimmune disorders,
CC reproductive disorders, and disorders of the placenta, and in the
CC assessment of the effects of exogenous compounds on the activity and
CC expression of proteins and nucleic acids associated with cell growth,
CC differentiation and death. CGDP polynucleotides are also used in a
CC claimed microarray and in a claimed method of generating an expression
CC profile of a sample

XX Sequence 1773 BP; 535 A; 334 C; 371 G; 533 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.35e-184 Length: 1773
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 8 Gaps: 1

US-10-077-111-13 (1-384) x AB224707 (1-1773)

QY 1 MetValLysLeuLleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
DB 60 ATGTGAAACTGATTTCACACATTAGCTGATGATGGTACAGATGTCACCTGTCCTTC 119
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuLysSerLeuArg 40
DB 120 TCTTTTCCCTCTGGCTACTTCTCTCTGACAAACAAATTCGCTGATCGTTACGT 179
QY 41 AspPheThrGluLeuPheHisSerProLeuLysPheHisThrTyralaValHisCysCys 60
DB 180 GACTTACTGAACTGCACATCTCCATTCAGTTTCATCTATGCTGTCCTCCTGCTGC 239
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB 240 TGTTTCTCCCTTCAGACATATTTTGGCATCGTTTCAACAGTGGTACCACCTGCTTA 239
QY 81 TrpAsnThrGluAsnGlyInMetLeuAlaValMetGluInProSerGlySerProVal 100
DB 300 TGGAACTAGTAAATGACAGATGCTGAGTGGAACAGCCTAGTGGCAGCCCTGTC 359
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
DB 360 AGGAGTTTGCAGATTTTCCAGACTCCACGTGTTTGGCACTCAGGGGACGCTGATGAAC 419
QY 121 ValValLeuTrpAsnAlaGlnSerTyLysLeuTyArgCysGlySerValLysAspGly 140
DB 420 GTGCTTTTGGGAATGACAGCTCATACAAATTATATGATGTGTATTAAGATGGC 479
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
DB 480 TCCTTGGCGGAGTGTGATTTTCTCTTAATGGAAGCTTTCTTTGCACTGGCTCCTCATGT 539
QY 161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
DB 540 GGGGATTTTAAACAGTGGGATGATAAATAGAGGTCTGATAGTGAAGAAAGACATGAT 539
QY 181 LeuGlyIleThrCysAspAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
DB 600 CTGGGAATTAACCTGCTGCGATTTTCTTTCACAGCCAGTTTCTGATGGAGAACAGGCTCT 659

QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleThrPheValSer 220
DB 660 CAGTTTTCGACTGGCATCATGTGGTCAAGATTGCGMGTGMAATTTGGATTTGTTCT 719
QY 221 PheThrHisIleLeu----- 225
DB 720 TTTTACCATATCTTTAGTGTTTGAATTAAATATATAAGATACACTGAGTGGCATGTGCT 779
QY 225 ----- 225
DB 780 CCTGTTCTGGCTTGTCTTTTCCATGATGGGCAGATCTAGTCTCAGGCTCAGTGCAT 839
QY 225 ----- 225
DB 840 AAGTGTGATGATATATATGATATCTAATACAGAAATATATCTTCACACATTGACTGAC 899
QY 225 ----- 225
DB 900 ACCAGGATATGCAACATTGTGCTTTTGGACCTTAATACCTTTTACTTGTCTACGTGTC 959
QY 226 -----AlaArg 228
DB 960 ATGGACAAAACAGTGAACATCTGGCAATTGACCTGGAACACTTTGCCAGCGAGAC 1019
QY 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValSerThrTrp 248
DB 1020 ACAGAACATCAGCTGAGCAATTTTCCGAAGATTGGTTCAGAGAGAGATCTTCACATCG 1079
QY 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePhePheMetCysHisGlnIleAspGly 268
DB 1080 CTTTGTGACAAAGATTAAAGATCTTGTGATTTTCAAGATGATTAACATTTGATGGA 1139
QY 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
DB 1140 AAAGAACTGTGAATCTTCAAAAGAAAGTCTGCTGATGATTTGAAATTTGAAATCTCTA 1199
QY 289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
DB 1200 GGACTCGTAGTAAAGTGTGAGGAAATTTGAAGAGCTCAGGACCAAGGTTAAATCCCTT 1259
QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLysLysAspPro 328
DB 1260 TCTTCAGGAATTCCTGAT 1319
QY 329 ValIleAlaSerAspGlyTyLysSerTyGluLysGluAlaMetGluLysIleThrPheSerLys 348
DB 1320 GTGATGCAATCAGATGCTGATATATATGAAAGAAAGCAATGAAATTTGATCAGACAA 1379
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1380 AAGAAACGTAAACAGTCCCATGACAAATCTTGTCTTCTTCAGCGGTACTTACACCAAT 1439
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
DB 1440 AGGACTCTGAAATATGSCCATTAATATGATGCTGGAGACACACCAAAAG 1487
RESULT 7
ID ADB63535 standard; cDNA; 1811 BP.
XX ADB63535;
XX 04-DEC-2003 (first entry)
DE Human cDNA encoding clone TEST120264530.
XX Human; sb; gene; pharmaceutical; diagnostic; gene therapy;
XX tissue regeneration; cell regeneration; membrane protein;
XX signal transduction-related protein; transcription-related protein;
XX osteoporosis; neurological disease; cancer; tumor.
OS Homo sapiens.
XX

Key	Location/Qualifiers
FT CDS	150..1580
FT	/*tag= a
FT	/product= "Clone TEST120264530 protein"
XX	
PN	EP1308459-A2.
XX	
PD	07-MAY-2003.
XX	
PE	28-MAR-2002; 2002EP-00007401.
XX	
PR	05-NOV-2001; 2001JP-00379298.
PR	25-JAN-2002; 2002US-00350978.
XX	
PA	(HELI-) HELIX RES INST.
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.
PI	Isoaga T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX	
XX	WPI: 2003-450961/43.
DR	P-PSDB; ADB65505.
XX	
PT	New polynucleotides and polypeptides, useful for developing a diagnostic
PT	marker or medicines for regulation of their expression and activity, or
PT	as targets of gene therapy.
PS	
XX	Claim 1; Page; 222pp; English.
XX	
CC	The invention discloses a polynucleotide comprising a sequence selected
CC	from 1970 fully defined nucleotide sequences which encode novel
CC	polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC	or its partial peptide, an antibody binding to the polypeptide or peptid
CC	of the polynucleotide, immunologically assaying the polypeptide or
CC	peptide of the polynucleotide by contacting the polypeptide or peptide
CC	with the antibody of the encoded protein, and observing the binding
CC	between the two, a transformant carrying the polynucleotide in an
CC	expressible manner and an antisense polynucleotide. The oligonucleotide
CC	is useful as a primer for synthesizing the polynucleotide, or as a probe
CC	for detecting the polynucleotide. The polynucleotides and encoded
CC	proteins are useful as pharmaceutical agents and many disease-related
CC	genes may be included in them, for developing a diagnostic marker or
CC	medicines for regulation of their expression and activity, or as targets
CC	of gene therapy. The genes are involved in tissue and/or cell
CC	regeneration. Membrane proteins, signal transduction-related proteins,
CC	transcription-related proteins, disease-related proteins and genes
CC	encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC	neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC	the activity or expression of the encoded protein to treat diseases. The
CC	sequence presented is a cDNA of the invention. Note: Some of the sequences
CC	data for this patent is not represented in the printed specification, but
CC	is based on sequence information supplied by the European Patent Office.
XX	
SO	Sequence 1811 BP; 520 A; 352 C; 399 G; 540 T; 0 U; 0 Other;
XX	
Al	Alignment Scores:
Pr	Prod. No.: 1,39e-184
Sc	Score: 1978.00
Sc	Length: 1811
Sc	Matches: 382
Sc	Conservative: 0
Sc	Best Local Similarity: 80.25%
Sc	Mismatch: 2
Sc	Query Match: 96.63%
Sc	Indels: 92
Sc	Gaps: 1
DB	
US	US-10-077-111-13 (1-384) x ADB65335 (1-1811)
QY	1 MetValysIeuIleIshIreIueIaAePHISGIyAePvAlAsnCySAlaPhe 20
DB	150 ATGCTGAACCTGATTCACACATTAGCTGATCATGTGAGCATGTCACCTGCTTC 209
QY	21 SerPheSerIeuIeuAlaThrCySSerIeuAaPpyIshIleAgluETrYSerIeuArg 40
DB	210 TCCCTTTCCTCTTGGCTACTGCTCTTGGACAAACATTGCGCTGACTGCTTACGT 269

QY	41	AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys	60
Db	270	GACTTTAAGTGAACGCCACATCTCCATTAAGTTTATACCTATAGCTGTCCACTGCTGC	329
QY	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
Db	330	TGTTTCCCCCTTCAGGACATATTTTGGCATTCGTGTTCAACAGATGGTATCAGCTGCTTA	389
QY	81	TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	100
Db	390	TGGAAATCTGAATAATGACAGATGCTGGCAGTGTGAGAACGCTTACTGGCAGCCCTGTC	449
QY	101	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr	120
Db	450	AGGGTTTGCCAGATTTTCCACAGACTCCAGCTGTTGGCATTCAGGGGACGCTGAAGACT	509
QY	121	ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly	140
Db	510	GTGGTTTGTGGAGATGACAGCTCATACAAATTATATGATGCTGGTACTGTTAAAGATGCC	569
QY	141	SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	570	TCCCTTGCGCGCATGTGCATTTTCTCCATAAGGAAGCTTCTTGTCACCTGCTCCTCAATGT	629
QY	161	GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGluLysAlaHisAsp	180
Db	630	GGTATTTTAACAGTGTGGATGATATAAATAGGTTGTGCATATGCTAAAGAACCATGAT	689
QY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu	200
Db	690	CTTGGAATTACCTGCTGCTGCATTTTCTTCCACGCACTTTCTGATGGAGAACAGTCTT	749
QY	201	GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer	220
Db	750	CAGTTTTCCTGACCTGGCATCATGTGTCAGAGATGGCCAAAGTCAAAATTTGGATTGTTCT	809
QY	221	PheThrHisIleLeu-----	225
Db	810	TTTACCATATCTTAAGCTTTGGAATTAATAATATAAGTACACTGAGTGGGCACTGTGCT	869
QY	225	-----	225
Db	870	CCTGTTCGGCTGTGCTTTTCCCATGATGGGAGATGCTAGTACTCAGGTCAGTGAT	929
QY	225	-----	225
Db	930	AAGTCTGTCAATAGTATATGATACTAATACTGAGATATACTTCACACATTGACTCAGCAC	989
QY	225	-----	225
Db	990	ACCAAGTATGTACACACTTGTGCTTTGGCACCTPATACCTTTTACTTGTCTACTGTTCA	1049
QY	226	-----AlaArgArg	228
Db	1050	ATGGAACAAAACAGTGAACATCTGGCAATTGACCTGGAAACACTTGTCCAAAGCAGAGAC	1109
QY	229	ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTyr	248
Db	1110	ACAAACATCATCGCTGAAGCAATTTTACCGAAGATTGTGCAAGACGATGCTCAACATGCG	1169
QY	249	LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly	268
Db	1170	CTTTGTGTCAACAAGTTTAAAGAATCTTGTTGGTATTTTCAAGATGATTAACATTGATGGA	1229
QY	269	LysGluLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGluSerLeu	288
Db	1230	AAAGAACCTGTGATCTTACAAAAGAAAGTCTGGCTGATATTTGAAATAATTGAAATCTCTA	1289
QY	289	GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu	308
Db	1290	GGACTTCGTAGTAAAGTCTGAGGAAAAATTGAGAGCTCAGGACCAAGGTTAAATCCCTT	1349

QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
DB 1350 TCTTCAGGAATTCCTGATGTAATTTATATGTCACATACTAGAGAACTTATGAAAGATCCG 1409
QY 329 ValIleAlaSerAspGlyIleTyrSerIleGluLysGluAlaMetGluMetTrpIleSerLys 348
DB 1410 GTCATGCGACATCAATGCTATTCATATGAAAGAACCAATGMAATTGGATCAGCGAA 1469
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1470 AAGAAACGTACAGGTCCCATGACCAATCTTCTTCTTCAGCGGACTTACACCAAT 1529
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
DB 1530 AGGACCTGAAATGGCCATCAATAGATGGCTGAGACACACCAAAAG 1577
RESULT 8
ID ADB47507 standard; cDNA; 1817 BP.
XX ADB47507;
XX ADB47507;
XX 04-DEC-2003 (first entry)
XX Human cDNA upregulated in dendritic cells SEQ ID NO 207.
XX es; gene; human; dendritic cells; high throughput; cancer;
XX infectious disease; autoimmune disease; allergy;
XX graft versus host disease; vaccine enhancing; gene therapy.
XX Homo sapiens.
XX US2003134283-A1.
XX 17-JUL-2003.
XX 03-OCT-2001; 2001US-00971392.
XX 03-OCT-2000; 2000US-0237652P.
XX (PETE/) PETERSON D P.
XX (PEAR/) PEARSON C I.
XX (COCK/) COCKS B G.
XX Peterson DP, Pearson CI, Cocke BG;
XX WPI; 2003-662509/62.
XX New combination comprises cDNAs that are differentially expressed in
XX dendritic cells useful for preparing a composition for diagnosing or
XX treating cancer, infectious disease, autoimmunity, allergy or graft
XX versus host disease.
XX Claim 1; SEQ ID NO 207; 28bp; English.
XX The invention relates to a combination comprising cDNAs that are
XX differentially expressed in dendritic cells (DC). Also included is a high
XX throughput method for detecting differential expression of one or more
XX cDNAs in a sample containing nucleic acids. The combination is useful for
XX preparing a composition for diagnosing, treating and monitoring the
XX treatment of cancer, infectious disease, autoimmunity, allergy or graft
XX versus host disease, or for enhancing a vaccine. The present sequence
XX represents a human cDNA upregulated in dendritic cells. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?docID=20030134283.
XX
XX Sequence 1817 BP; 519 A; 373 C; 383 G; 542 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 139e-184 Length: 1817
XX Score: 1978.00 Matches: 382
XX Percent Similarity: 80.25% Conservative: 0

Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 10 Gaps: 1
US-10-077-111-13 (1-384) x ADB47507 (1-1817)
QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
DB 148 ATGTGAACCTGATTCACACATTAAGCTGATCATGGGAGCATGTCAACTGCTGCTTC 207
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleValGluLysSerLeuVal 40
DB 208 TCCCTTTCCCTCTGGCTACTGCTCTCTTGGACAAACAAATTCGCTGACTGCTTACGT 267
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheIleThrTyrAlaValHisCysCys 60
DB 268 GACTTACTGMACTGGCACATCTCCATTGMACTTTCATACCTATCTGCTCCACTGCTCG 327
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB 328 TGTTCCTCCCTTCAGACATATTTTGGCATCGTGTCAACAGATGTACCACTGCTCTTA 387
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
DB 388 TGGAAATPACTGAAATGAGACAGATGCTGGCAGATGGAACAGCTTATGGCAGCCCTGTG 447
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
DB 448 AGGGTTTGGCAGTTTCCCAAGCTCCACAGCTCAGCTGTGGCATCAGGGCAGCTGATGA 507
QY 121 ValValLeuTrpAsnAlaGlnSerIleLysLeuTyrArgCysGlySerValLysAspGly 140
DB 508 GTGGTTTGGGAATGACAGATCATCAAAATTATATAGATGTGGTATTAAGATGGC 567
QY 141 SerLeuAlaAlaLysAlaPheSerProAsnGlySerPheValThrGlySerSerCys 160
DB 568 TCCCTGGCGGACAGTCAATTTCTCTTAATGGAAGCTTTCTTGTCACGTCTCTCATGT 627
QY 161 GlyAspLeuThrValTrpAspAspLysMetCysCysLeuHisSerGlyIleValAsnAsp 180
DB 628 GGTGATTTTAACTGATGCGGATGATTAATAAGAGTGTCTGCATATGTGAAAAGCACTGAT 687
QY 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
DB 688 CTGGAAATTACCTGCTGCATTTTCTTCACAGCCAGTTTCTGATGAGAACAAAGGCTCTT 747
QY 201 GlnPheAspArgLeuAlaSerCysGlyGlnAspCysGlnValIleTrpIleValSer 220
DB 748 CAGTTTTCGACTGCGCATCATGTGTGTCAGATTTGCCAAAGTCMAAATTTGATTTGTTCT 807
QY 221 PheThrHisIleLeu----- 225
DB 808 TTTAACCATATCTTAACTTTTGAATTAATAATATAAAGTACACTGAGTGGCACTGTGCT 867
QY 225 ----- 225
DB 868 CTGTTTGGCTGTGCTTTTCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGAT 927
QY 225 ----- 225
DB 928 AAGCTGTCTATGATATATGATATACTAGATATACTCAGATATATCTTACACTCAGCAC 967
QY 225 ----- 225
DB 988 ACCAGTATGTCACTACTGTGCTTTTGCACCTAATACCTTTTACTGTGCTACTGTTCA 1047
QY 226 -----AlaArgArg 228
DB 1048 ATGACAAACACAGTGAACATCTGGCAATTTGACCTGGAAACACTTTGCCAACAGAGAGC 1107
QY 229 ThrGlnHisGlnLeuLysGlnPheThrGluAspTrpSerGlnGluValIleSerThrTrp 248
DB 1108 ACAGAACATCAGCTGAAGCAATTTACCGAAGATTTGTCAGAGGAGATGTCTCAACATGG 1167

OY	249	LeuCySA1aG1aSPLeuLySaSPLeuVal1G1y1IlePheLySeMetSnaEn11eaSPGly	268
Db	1168	CTTGTGGCAACAAGATTAAAGATCTTGTGGATATTTTCAAGATGAATTAACATTGATGGA	1222
OY	269	LysG1uLeuLeuAsnLeuThrLysG1uSerLeuAlaSPaSPLeuLyS1IeG1uSerLeu	288
Db	1228	AAAGAAGCTGTTGAATCTTACCAAAAGAAAGCTGGCTGATGATTTGAAAAATTGAATCTCTA	128
OY	289	G1yLeuA1gSerLysValLeuArgLyS1IeG1uLeuArgThrLysValLysSerLeu	308
Db	1288	GGACTCGCGACGTAAAGTGCCTGAGGAAAAATTGAAAGCTCAGAGCCAAAGCTTAAATCCCTT	1344
OY	309	SeSerG1y1IleP1aSPG1uPhe1IeCySP1r1IeThrArgG1uLeuMetLysASPPro	328
Db	1348	TCTTCAGGAATCTCCTGATGAATTTTATATGTCCAATTAAC1aGAAACCTTAAGAAGATCCG	1404
OY	339	Val1IeAlaSerASPQ1yTy1SerTyrg1uLySg1uAlaMetG1uAsnT1p1IeSerLys	348
Db	1408	GTCATCGCATCAGATGGCTATTTCATATGAAGAAAGCAATGAAAAATTGCATCAGCAA	1464
OY	349	LysLySA1gTh1SerP1roMetThraSnLeuValLeuProSerAlaValLeuTh1rProAsn	368
Db	1468	AAGAAGACGTAAAGTCCCACTGACAAATCTTGTTCTTCTTCACGCGTACTTACACCAAT	1524
OY	369	ArgTh1rLeuLysMetAla1IeAsnArgT1pLeuG1uTh1rG1uLys	384
Db	1528	AGGACTCTGAAAAATGGCCATCAATAGATGGCTGGAGACACCAAAAG	1575
RESULT 9			
AA158876			
ID	AA158876	standard; cDNA; 1844	Bp.
AC	AA158876;		
XX			
XX	22-OCT-2001	(first entry)	
XX			
DE	Human polynucleotide seq ID NO 1079.		
XX			
KW	Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathic; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Dreger Syndrome; chemotactic;		
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;		
XX	leukemia; ss.		
OS	Homo sapiens.		
XX			
PN	WO200153312-A1.		
XX			
PD	26-JUL-2001.		
XX			
PF	26-DEC-2000; 2000MO-US034263.		
XX			
XX	23-DEC-1999; 99US-00471275.		
PR	21-JAN-2000; 2000US-00488725.		
PR	25-APR-2000; 2000US-00553117.		
PR	20-JUN-2000; 2000US-00598042.		
PR	19-JUL-2000; 2000US-00620312.		
PR	03-AUG-2000; 2000US-00653450.		
PR	14-SEP-2000; 2000US-00662191.		
PR	19-OCT-2000; 2000US-00693036.		
PR	29-NOV-2000; 2000US-00727344.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,		
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q,		
PI	Zhou P, Goodrich R, Drmanac RT,		
XX			
DR	WPI. 2001-442253/47.		
DR	P-PSDB; AAM39720.		
XX			

PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX
XX
PS Claim 1; SEQ ID NO 1079; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA38642-AA62213) with neurotropic,
CC immunosuppressant and cytotostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemoclastic/chemokine activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

Alignment Scores:

Pred. No.:	1,42e+184	1844
Score:	1978.00	382
Length:		
Matches:		
Conservative:	0	0
Mismatches:	2	2
Best Local Similarity:	80.258	
Query Match:	96.634	92
DB:	4	1
Gaps:		

US-10-077-111-13 (1-384) X AAI58876 (1-1844)

QY	1	MetValIyLSleuILH:sthrLeuLaaspbH:sgLYaspAaspValaInCyCsYsaIaPhe	20
Db	164	ATGGGAAACATGATTCCACACATTAGCTGATCTAGGAGACGATGTCAACTGCTGCTTC	2232
QY	21	SerPheSerLeuLeuLaIaThrCySerLeuAapLyThrILeagYleuTyrSerLeuAry	40
Db	224	TCCTTTTCCCTCTTGCTGATCTGCTCCCTTGACAAACAAATTCGCTGTATCTGTTACGT	2838
QY	41	AspPheThrGluLeuProHissSerProdeuLySpheniEthrTyrrAlaValHISCyS6CyS	60
Db	284	GACITTAAGTGAACCTGCACATCTCCATGGAAGTTTCATACCTATGCTGTCCACTCTGC	3438
QY	61	CysPheSerProSerGlyHISrIleLeuLaIaSerCySerThrAspGlyThrThrValLeu	80
Db	344	TGTTTCTCCCTTCAGACATATTTTGGCATGTGTTCACACAGATGATACCATCTTCTTA	4030
QY	81	TryPanthrGluAsnGlyGlnmetLeuLaIaMetGluGlnProSerGlySerProVal	100
Db	404	TGGATTAAGTGAAGAAATGACAGATGCTGGCAGATGAGAAACAGCTATGTGGACACCCCTGTG	4638
QY	101	ArgValCysGlnPheSerProAspSerThrCysLeuLaISerGlyAlaIaaspGlyThr	120
Db	464	AGGGTTTCCAGGTTTTCCCCACAGCTCCACAGTGTGGCTTCAGAGGGCAGCTGATGGAACT	5238
QY	121	ValValIleuThrPanthAlaGlnserTyrlsLeuTyrrArgCysGlySerValIysAspGly	140
Db	524	GTTGTTTGTGGAAATGACACAGTCATACAAATTAATATAGATGGTGAAGTGTAAAGATGGC	5838
QY	141	SerLeuLaIaLaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	584	TCCTTTGGGGGCGATGTGCATTTTCTCTTAATGGAAGCTTTTGTCTCATCTGCTCTCATGT	6438
QY	161	GlyAspLeuThrValITrpAspAspIysMetArgCysLeuHISerGlyIuYsaIaHISasp	180
Db	644	GGTGATTTAACAGTGTGGGATGATATAAATGAGGTGCTCATATGTAATAAAGACATGAT	7038
QY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerIAspGlyGluGlnGlyLeu	200
Db	704	CTTGAATTAATCTGTGTGGATTTTCTTCACAGCAGATTTCGTGATGGAAACAAAGGCTTT	7638


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Db 524 GTGCTTTTGTCAGATGCACGTCTACAAATATATAGATGTGTAAGTTAAAGATGC 583
Qy 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db 584 TCCCTTGGCGGCGATGTGCAATTTTCTCTAATGGAAGCTTCTTGTCCAGCTGCTCTCATGT 643
Qy 161 GlyAspLeuThrValTTPAspAspLeuMetArgCysLeuHisSerGluValHisAsp 180
Db 644 GGTATTTTAAACAGTGTGGATGATPAAATGAGGTGTGCAATGATGAGAAAGCAATGAT 703
Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 704 CTTGGAATTACTCTGCTGCGATTTTCTTTCACAGCAGTTTCTGATGAGAAACAAGTCTT 763
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValIleTyrIleValSer 220
Db 764 CAGTTTTCAGCTGCGATCATGTGTGTCAGATTTGCCAAGTCAAAATTTGGATTGTTCT 823
Qy 221 PheThrHisIleLeu----- 225
Db 824 TTATCCCATATCTTATGGTTTGAATPAAATATPAAAGTACATGAGTGGCAGCTGTGCT 883
Qy 225 ----- 225
Db 884 CCTGTTCTGCGTGTGCTTTTCCCATGATGGGAGAGATGCTAGTCTCAGGCTCAGTGAT 943
Qy 225 ----- 225
Db 944 AAGCTGTGATAGTATATGATATCAATPACTGAGATATACTTACACATGACTCAGAC 1003
Qy 225 ----- 225
Db 1004 ACCAGTATGTCAACAATTGTGCTTTTGCACTTAATACCTTTTACTTGTACTGTTC 1063
Qy 226 -----AlaArgArg 228
Db 1064 ATGACAAACACAGTCAACATCTGCAATTTCACCTGGAACACTTGGCAACAGAGAGC 1123
Qy 229 ThrGlnHisGlnLeuValGlnPheThrGlnAspTyrSerGlnGluValIleSerThrTyr 248
Db 1124 ACAGAACTCAGCTGAGGCAATTTACCGAAGATTGTGTGAGAGAGAGATGTCTCAACATGG 1183
Qy 249 LeuCysAlaGlnAspLeuValGlyIlePheLeuMetAsnHisIleAspGly 268
Db 1184 CTTGTGCAACAAGATTAAAGATCTGTGTATTTTCAAGATGAATPAAACATTGATGGA 1243
Qy 269 LysGlnLeuLeuAsnLeuThrGlySerLeuAlaAspAspLeuValIleGlySerLeu 288
Db 1244 AAAAAGACTGTTGAATCTTACAAAGAAAGTCTGCTGATGATTTGAAATTTGAATCTTA 1303
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGlnGluLeuArgThrLysValLysSerLeu 308
Db 1304 GGACTGCGTAGTAAAGTGTGAGGAAATTAAGAGCTCAGAGCAACAAGTTAAATCCCTT 1363
Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db 1364 TCTTCAGGAATTTCCGATGAAATTATATATGTCCAATPAAAGAACTTATPAAAGATCCG 1423
Qy 329 ValIleAlaSerAspGlyTyrSerTyrGlnLysGlnAlaMetGlnAsnTyrIleSerLys 348
Db 1424 GTCAATCCGATCAGATGGCTATTTCAATGAAAAGAAAGAAAGTGAATTTGATCAGCAA 1483
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1484 AAGAAACCTACAGTCCCATACAAATCTTGTCTTCTTCAAGCGGTCTTACACCAAT 1543
Qy 369 ArgThrLeuLysMetAlaIleAsnArgThrLeuGluThrHisGlnLys 384
Db 1544 AGGACTCTGAAAATGGCCATCATATGATGTGCTGAGACACACCAAG 1591
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ID ADB48858 standard; cDNA; 1844 BP.
XX
AC ADB48858;.
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA seq ID NO 768.
XX
KW ss; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
PN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PE 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIU/) LIU C.
PA (ASUNDI/) ASUNDI V.
PA (DRMANAC/) DRMANAC R T.
XX
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX
DR WPI; 2003-678194/64.
XX
PT New polynucleotide, useful for treating diseases e.g., cancer or
PT neurodegenerative diseases.
XX
PS Claim 1; SEQ ID NO 768; 99bp; English.
XX
CC The invention relates to a polynucleotide comprising a sequence given in
CC the specification, or its mature protein-coding portion, or its
CC complement. The polynucleotide is useful for treating diseases e.g.,
CC cancer or neurodegenerative diseases and many others listed in the
CC specification. The present sequence represents a novel human cDNA. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPRO
CC at seqdata.uspro.gov/sequence.html?docid=20030104529.
XX
SQ Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 142e-184 Length: 1844
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: Gaps: 1
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Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
Db 164 ATGTGAAAGATGATTCACACTTAGTGTGATGATGATGATGATGATGATGATGATGATGAT 223
Qy 21 SerPheSerLeuLeuAlaThrCysSerSerLeuAspLysThrIleArgGluTyrSerLeuArg 40
Db 224 TCCCTTTCCCTCTTGGGTACTGTCTCTTGGACAAACAAATTCGCTGTACTGTTACGT 283
Qy 41 AspPheThrGlnLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
Db 284 GACTTTACTGACACGCCACATTTCTCCATTTGAAGTTTATATACATGCTGTCCATGCTGCG 343
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 344 TGTTCCTCCCTTCAGACATATATTTTGGCATCGTGTCAACACAGTGTGATCACTGTCTTA 403
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QY      81  TTPAsnThnGluAengIyGImoCLeuAlaValMeGluGlnProSerGlySerProVal 100
Db      404  TGGAAATACtAAAAATGACAGATCGTCAGTATGAGAACGCTTACTGGCAGCCCTGTG 463
QY      101  ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
Db      464  AGGGTTGGCCAGTTTCCAGACTCCACGCTGTTGGCATCAGGGGAGCGCTGATGAACT 523
QY      121  ValValLeuThrPheAlaGlnSerThrLeuValThrGlyCysGlySerValLysAspGly 140
Db      524  GTGGTTTGTGGAAATGACAGTCAATACAAATTAATATGATGGTACTGTTAAAGATGSC 583
QY      141  SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db      584  TCCTGGCGGCACTGTGATTTCTCCTAATGGAAGCTCTTTGTGCATGGCTCCTCATGT 643
QY      161  GlyAspLeuThrValTTPAspAspLysMetArgCysLeuHisSerGlyValAlaHisAsp 180
Db      644  GGTGATTTAAACAGTGTGGATGATAAATAGAGTGTCTGCATAGTGAATAAGCACATGAT 703
QY      181  LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db      704  CTTCGAAATACCTGCTGCGAATTTCTTTCACAGCCAGATTTCTGATGGAGAACAGGCTT 763
QY      201  GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleThrPileValSer 220
Db      764  CAGTTTTCGACCTGGCATGTGTCAGAGATTGGCAAGTCAAAATTTGGATTGTTCT 823
QY      221  PheThrHisIleLeu----- 225
Db      824  TTTTACCATATCTTAGGTTTGAATTAAAAATATAAAGTACACTGAGTGGCACTGTGCT 883
QY      225  ----- 225
Db      884  CCTGTTCTGCTGTGCTTTTCCCATGATGGGAGATGCTAGTCTCAGGAGTACGTGAT 943
QY      225  ----- 225
Db      944  AAGCTGTCAATGATATGATACTAATACTAGAGAATATACTTGCACAGATTGACTCAGCAC 1003
QY      225  ----- 225
Db      1004  ACCAGATATGTCACAACTGTGCTTTTGCACCTAATACCTTTACTTGTCTACTGTTCA 1063
QY      226  -----AlaArgArg 228
Db      1064  ATGGACAAAACAGTGAAATCTGGCAATTGGACCTGGAAAACCTTGGCCAAAGAGAGAC 1123
QY      229  ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValValSerThrTrp 248
Db      1124  ACAGAACATCAGCTGAAGCAATTTTACCGAAGATTGGTCAGAGGAGATGTCCTCAACATGG 1183
QY      249  LeuCyAlaIleGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAlaHisAspGly 268
Db      1184  CTTTGTGCACAAAGATTAAAGATCTTGTGTATTTTCAAGATGAATAACATTGAAGGA 1243
QY      269  LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
Db      1244  AAGGAATCTGTTGAATCTTACAAAGAAAGTCTGGCTATGATTTGAAAAATTTGAATCTCTA 1303
QY      289  GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
Db      1304  GGAAGTGTGTAAGAGTGAAGAAAATTGAAGAGTCAAGAACCAAGTTAAATCCCTT 1363
QY      309  SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db      1364  TCTTCAGGAATCTCTGATGAATTAATATGTCATATACTAGAGAACTTATCAAAAGATCCG 1423
QY      329  ValIleLeuAspArgLysThrSerThrGluLysGluAlaMetGluAsnThrPileSerLys 348
Db      1424  GTCATGCATCAGATGGCTATTCTATATGAAGAAAGAACCAATGGAAATTTGATCAGCAAA 1483

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QY      349  LysLysArgThrSerProMetThrPheLeuValLeuProSerAlaValLeuThrProAsn 368
Db      1484  AAGAAACGTACAAAGTCCCATGACAAATCTTCTTCTTCCAGCGGTACTTACACCAAAAT 1543
QY      369  ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
Db      1544  AGGACTCTGAAATGGCCATCATATAGATGCTGCAGACACACCAAAAG 1591

RESULT 12
AAD45076
ID  AAD45076 standard; DNM; 1908 BP.
XX
AC  AAD45076;
XX
DT  27-DEC-2002 (first entry)
XX
DE  Human RET16.3 splice variant DNM.
XX
KW  Human; RET16; intracellular signal; inflammation-related disease; asthma;
KW  rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
KW  transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
KW  inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
KW  inactive respiratory distress syndrome; cardiac; ulcerative colitis;
KW  autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
KW  cellular migration disorder; cell proliferation disorder; calcification;
KW  hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
KW  cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
KW  thalassemia; vasotropic; gene; ds.
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  CDS 136..1644
FT  /tag= a
FT  /product= "Human RET16.3 splice variant protein"
XX
XX  WO200266494-A2.
XX
PD  29-AUG-2002.
XX
PF  15-FEB-2002; 2002WO-US005162.
XX
PR  16-FEB-2001; 2001US-0269366P.
PR  29-MAY-2001; 2001US-0294181P.
XX
PA  (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI  Toddard CG, Finger JN, Rillema J;
XX
XX  WPI; 2002-682760/73.
XX  P-PSDB; AAE28168.
XX
PT  New human, mouse or rat RET16 gene and proteins, involved in
PT  intracellular signaling cascade, useful for in gene therapy, particularly
PT  for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancer,
PT  tumors or neoplasms.
XX
PS  Claim 1; Page 168-169; 175pp; English.
XX
XX  The invention relates to human, mouse or rat RET16 genes and proteins,
XX  involved in intracellular signaling cascade. The RET16 protein or
XX  polynucleotide is useful for treating an inflammation-related disease or
XX  disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
XX  asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
XX  tissue transplants, chronic obstructive pulmonary disease, inflammatory
XX  bowel disease, Crohn's disease, ulcerative colitis, incurable respiratory
XX  distress syndrome, systemic lupus erythematosus, autoimmune disease,
XX  cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
XX  disease or disorder also includes disorders associated with aberrant
XX  activation of the TNF-alpha pathway, disorders associated with aberrant
XX  cellular migration, proliferation, metastasis, juvenile idiopathic
XX  arthritis, haematogenous metastases of tumour cells, hyperinsulinaemia,
XX  diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,

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CC tumour progression, Wegener's granulomatosis, stem cell transplantation
 CC complications, ischemia-reperfusion injury, chalassemia, acute lung
 CC injury, graft rejection, ischemic heart, coronary artery calcification
 CC or allergic inflammation, RET16 DNA is used in gene therapy. The present
 CC sequence is human RET16.3 splice variant DNA

XX Sequence 1908 BP; 550 A; 399 C; 405 G; 554 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.4e-182 Length: 1908
 Score: 1958.00 Matches: 382
 Percent Similarity: 76.29% Conservative: 1
 Best Local Similarity: 76.10% Mismatches: 1
 Query Match: 95.65% Indels: 118
 DB: 6 Gaps: 2

US-10-077-111-13 (1-384) x AAD45076 (1-1908)

QY 1 MetValIysLeuIleHISThrLeuAlaAspHisGlyAspAspValAsnCySAlaPhe 20
 Db 136 ATGGTGAACGATTCACACATTAAGCTGATCATGTGACGATGTCACACTGCTGCTTC 195
 QY 21 SerPheSerLeuLeuAlaThrCySerLeuAspLysThrIleArgLeuTySerLeuArg 40
 Db 196 TCTTTTCCCTCTGGCTACTTGGCTCTGTCGACAAACAATTGCGCTGTACTCTGTTAGCT 255
 QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyAlaAlaHisCySAs 60
 Db 256 GACCTTACTGAACGCCACATTCCTCATGAAATTCATACCTTACCTGCTGCTGCTGCTG 315
 QY 61 CyPheSerProSerGlyHisIleLeuAlaSerCySerThrAspGlyThrValLeu 80
 Db 316 TGTTCCTCCCTTACGACATATTTTGGCATCGTGTACACAGATGATACACACTGTCTTA 375
 QY 81 TrpAsnThrGluAsnGlyGlyMetLeuAlaValMetGluGlnProSerGlySerProVal 100
 Db 376 TGGAACTACTGAAATGACACAGATGCTGGCAGTGTGAAACAGCTTACGAGCCCTGTG 435
 QY 101 ArgValCySglnPheSerProAspSerThrCySLeuAlaSerGlyAlaAlaAspGlyThr 120
 Db 436 AGGGTTGGCGGATTTTCCAGACTCCACGCTTTGGCATGAGGGCGCTGATGAACT 495
 QY 121 ValValLeuThrPAsnAlaGlnSerTyTrpLeuTyArgCySglnSerValLysAspGly 140
 Db 496 GTGCTTTTGTGATGACACAGTCACTACAAATTATATAGATGTGTGATTAAGATGCG 555
 QY 141 SerLeuAlaAlaCySAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
 Db 556 TCCTTGGCGGATGTGATTTTCTCTTAATGGAAGCTTCTTGTACATGGCTCTCATGT 615
 QY 161 GlyAspLeuThrValTrpAspAspLysMetArgCySLeuHisSerGluLysAlaHisAsp 180
 Db 616 GGTGATTTTACAGCTGGGATGATAAATGAGTGTCTGCAATGAGAAAAAGCATATAT 675
 QY 181 LeuGlyIleThrCySAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
 Db 676 CTGGAAATTACCTGCTGCGATTTTCTTCAAGCCAGTTTCTGAGAGGAACAAGGCTT 735
 QY 201 GlnPhePheArgLeuAlaSerCySglnAspCySglnValLysIleTrpIleValSer 220
 Db 736 CAGTTTTTTCAGCTGGCATCATGTGTGAGATTGCCAAAGTCAAAATTTGGATTGTTCT 795
 QY 221 PheThrHisIleLeu----- 225
 Db 796 TTTTACCCATATCTTGAAGTTTGAATTAATAAAGTACACTGAGTGGCACTGTGCT 855
 QY 225 ----- 225
 Db 856 CCTGTCTGCGCTTGTGCTTTTCCCATGATGGGCAAGTCTAGTCTCAGGGCTCAGTGAT 915
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 Db 916 AAGTCTGTGATGATATGATACTAATACTGAGAAATATATCTTACACACTGACTGACAC 975

QY 225 ----- 225
 Db 976 ACCAGTATGTACACACTTGTGCTTTTGGCACTTAATACCTTTTACTTGTCTACTGTTC 1035
 QY 226 -----AlaArgArg 228
 Db 1036 ATGGCAAAACAGTGAACATCTGGCAATTGACCTGGAAACACTTTGGCAAGGCGC 1095
 QY 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTrp 248
 Db 1096 ACAGAACATCAGCTGAAGCAATTTTACCGAAGATTGGTCAGAGGAGCATGTCTCAACATGG 1155
 QY 249 LeuCySAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
 Db 1156 CTTTGTGCACAGATTTTAAAGATCTGTGTGTGATTTTTCAGATGATTAACATTTGATGGA 1215
 QY 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIle----- 285
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 QY 285 ----- 285
 Db 1276 CCTCTGGCATGTCATCCTCACTGACGACTTCAACTCTGGGCTCAAGTGAATCCTCTTA 1335
 QY 286 -----GluSerLeuGlyLeuArgSerLysValLeuArgLysIleGluGluLeuArg 302
 Db 1336 CCTCGGCTCAATCTTCAAGACTGTGAGTAAGTGTCTGAGAAATTTGAAGAGCTCAGG 1395
 QY 303 ThrLysValLysSerLeuSerSerGlyIleProAspGluPheIleCySProIleThrArg 322
 Db 1396 ACCAAGTTAAATCCCTTCTTCAGAAATTCCTGATGAATTTATATGTCATTAACATA 1455
 QY 323 GluLeuMetLysAspProValIleAlaSerAspGlyTyTrpSerTyGluLysGluAlaMet 342
 Db 1456 GAACCTTAGAAGATCCGGTGCATGCAATGATGCTATTCATATGAAAGGAAGCAATG 1515
 QY 343 GluAsnTrpIleSerLysLysLysArgThrSerProMetThrAsnLeuValLeuProSer 362
 Db 1516 GAAATTTGATCACAACAAAGAAACGTAACAGTCCATGACAAATCTTGTCTTCTCTTCA 1575
 QY 363 AlaValLeuThrProAsnArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHis 382
 Db 1576 GCGGTACTTACCAAAATAGGACTGTGAAATAGCCATCAATAGATGCTGGAGACAC 1635
 QY 383 GlnLys 384
 Db 1636 CAAAAG 1641
 RESULT 13
 AA164914
 ID AA164914 standard; cDNA; 1623 BP.
 AC AA164914;
 XX
 AC
 DT 04-DEC-2001 (first entry)
 XX
 DE Beta-transducin 41 coding sequence.
 XX
 KW Beta-transducin 41; cancer; HIV infection; gene therapy; ss.
 XX
 OS unidentified.
 XX
 CN1300734-A.
 XX
 PN 27-JUN-2001.
 XX
 PD 21-DEC-1999; 99CN-00124285.
 XX
 PE 21-DEC-1999; 99CN-00124285.
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 FR 21-DEC-1999; 99CN-00124285.
 XX
 PA (UVFU-) UNIV FUDAN.
 XX

QY 384 s 384
Db 262 A 262
RESULT 15
ID ADM19385
ADM19385 standard; cDNA; 1686 BP.
XX
AC ADM19385;
XX
DT 20-MAY-2004 (first entry)
XX
DE Novel human channel/transporter gene #182.
XX
KW da; gene; immunosuppressive; antiarthritic; antiheumatic;
KW antiapoptotic; cytoskeletal; cardiac; vasotropic; cerebroprotective;
KW neotropic; neuroprotective; antibacterial; virucide; fungicide;
KW optalmological; gene therapy; channel/transporter protein;
KW rheumatoid arthritis; neoplasm; cardiac arrest; cerebrovascular disorder;
KW cerebral ischemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.
XX
OS Homo sapiens.
XX
PN WO200154472-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001307.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 17-NOV-2000; 2000US-0249214P.
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PR 17-NOV-2000; 2000US-0249216P.

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XX	PR	01-DEC-2000;	2000US-0250160P.
XX	PR	01-DEC-2000;	2000US-0250319P.
XX	PR	05-DEC-2000;	2000US-0251030P.
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XX	PR	05-DEC-2000;	2000US-0256719P.
XX	PR	06-DEC-2000;	2000US-0251479P.
XX	PR	08-DEC-2000;	2000US-0251856P.
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XX	PR	11-DEC-2000;	2000US-0254097P.
XX	PR	05-JAN-2001;	2001US-0259678P.
XX	PA		
XX	PA	(HUMA-)	HUMAN GENOME SCI INC.
XX	PA		
XX	PI	Rosen CA,	Barash SC, Ruben SM;
XX	PI		
XX	DR	WPI;	2001-476159/51.
XX	DR	P-PSDB;	ADMI9864.
XX	PT		
XX	PT	Isolated nucleic acid molecule encoding a channel/transporter protein is used in preventing, treating or ameliorating a medical condition.	
XX	CS	Claim 1;	SEQ ID NO 192; 8099p; English.

The invention relates to an isolated nucleic acid molecule encoding a channel/transporter protein or sequences at least 95% identical to a these. The nucleic acids and proteins encoded by them are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. This sequence corresponds to a gene of the invention.

SQ Sequence 1686 BP; 485 A; 348 C; 353 G; 500 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.2e-159	length:	1666
Score:	1715.50	Matches:	335
Percent Similarity:	70.38%	Conservative:	0
Best Local Similarity:	70.38%	Mismatches:	2
Query Match:	83.81%	Indels:	139
DB:	5	Gaps:	2

US-10-077-1.11-13 (1-384) X ADM19385 (1-1686)

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Db	210	TCCCTTTTCCCTTGGCTGACTTGGCTCTCTTGGACAAACAAATGGCCGTGACTGTTAAAGCT	269
QY	41	AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys	60
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QY	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu	80
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QY	141	SerLeuAlaAlaCysAlaPheSerProAspGlySerPhePheValThrGlySerSerCys	160
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Db	1170	CTTTGTGACACAAGATTTAAAGATCTTGTGTGATTTTTCAGAGATGATATACATTGATGGA	1229
QY	269	LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu	288
Db	1230	AAAGACACTGTGATCTTTACAAAGAAAGTCTGGCTGATGATTTGAAAAATT-----	1280

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Search completed: October 25, 2005, 02:15:57
Job time : 512 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 04:11:04 ; Search time 3795 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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4: gb_om: *
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6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
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13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	893.4	70.2	1919	6 AK129983	Homo sapi
5	890.2	70.0	1811	6 AK748164	Sequence
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7	878.8	69.1	1996	6 CO491312	Sequence
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9	478.6	37.6	1291	6 AX076755	Sequence
10	474.6	37.3	2130	10 BC061948	Mus muscu
11	436	34.3	1547	10 BC050792	Mus muscu
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13	430	33.8	1470	9 AC008277	Homo sapi
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15	335	26.3	446	6 CO473162	Sequence
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17	331.6	26.1	366	6 CO135438	Sequence
18	331.6	26.1	366	6 CO218732	Sequence
19	331.6	26.1	366	6 CO294537	Sequence

C 20	331.6	26.1	366	6	CO311208	Sequence
C 21	329.8	25.9	409	6	CO482331	Sequence
C 22	328.8	25.8	441	6	CO503452	Sequence
C 23	328.8	25.8	441	6	CO512287	Sequence
C 24	297	23.3	297	6	CO109842	Sequence
C 25	297	23.3	297	6	CO148540	Sequence
C 26	297	23.3	297	6	CO231810	Sequence
C 27	297	23.3	297	6	CO307124	Sequence
C 28	297	23.3	297	6	CO344013	Sequence
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C 30	276.8	21.8	315463	2	AC122070	Sequence
C 31	275.4	21.7	196403	2	AC102767	Mus muscu
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C 36	179.6	14.1	466	6	CO219679	Sequence
C 37	179.6	14.1	466	6	CO258151	Sequence
C 38	179.6	14.1	466	6	CO295485	Sequence
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C 44	176.8	13.9	180	6	CO270754	Sequence
C 45	176.8	13.9	180	6	CO308036	Sequence

ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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JOURNAL
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AUTHORS
TITLE
JOURNAL
USA

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BC029520
BC029520.1 GI:20810486
MGC.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Srausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.H., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udén, T.B., Toshitoki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Adams, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
Mckernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, X., Gibbs, R.A.,
Vallion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Raney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1564)
Srausberg, R.
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palikofers, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki
Toshituki and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 48 Row: 0 Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 22749102.
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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1252; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION Sequence 768 from patent US 6569662.
ACCESSION AR339277
VERSION AR339277.1 GI:33726134
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1844)
AUTHORS Tang, Y.T., Zhou, P. and Dermanac, R.T.
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JOURNAL Patent: US 659662-A 768 27-MAY-2003;
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ORIGIN

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Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

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QY 876 GATCTTGTGCTATTTTCAAGATGATTAATGATGATGATGATGATGATGATGATGATGAT 935
DB 1205 GATCTTGTGCTATTTTCAAGATGATTAATGATGATGATGATGATGATGATGATGATGAT 1264
QY 936 AAAGAAAGTCTGCTGATGATTTTGAATTTGAAATCTCTAGACTGCTGCTGCTGCTGCTG 995
DB 1265 AAAGAAAGTCTGCTGATGATTTTGAATTTGAAATCTCTAGACTGCTGCTGCTGCTGCTG 1324
QY 996 AGGAAATTTGAAGAGCTCAGAGCAGCAAGTTAAATCCCTTTCTTCAAGATTTCTGATGAA 1055
DB 1325 AGGAAATTTGAAGAGCTCAGAGCAGCAAGTTAAATCCCTTTCTTCAAGATTTCTGATGAA 1384
QY 1056 TTTATATGCTCAATTAATAGAGAACTTAAGAAATCCGCTGCTGCTGCTGCTGCTGCTGCT 1115
DB 1385 TTTATATGCTCAATTAATAGAGAACTTAAGAAATCCGCTGCTGCTGCTGCTGCTGCTGCT 1444
QY 1116 TCATATGAAAAAGAGCAATGAAAAATTTGATGACGAAAAAGAAACCTGACAGTCCCATG 1175
DB 1445 TCATATGAAAAAGAGCAATGAAAAATTTGATGACGAAAAAGAAACCTGACAGTCCCATG 1504
QY 1176 ACAATATTTTCTTCTTCTTCAAGCGGCTACTTACACCAATATGAGCTCTGAAAAATGGCCATC 1235
DB 1505 ACAATATTTTCTTCTTCTTCAAGCGGCTACTTACACCAATATGAGCTCTGAAAAATGGCCATC 1564
QY 1236 AATGATGCTGAGAGACACCAAAAGTAAA 1266
DB 1565 AATGATGCTGAGAGACACCAAAAGTAAA 1595

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RESULT 3
CQ729621 1254 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 15555 from Patent WO02068579.
ACCESSION CQ729621
VERSION CQ729621.1 GI:42301208
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kils, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 15555 06-SEP-2002;
PB Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1..1254
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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QY	138	GATCATGCTGACGATGCTCAACCTGCGTGTGCTTCTCTTCCCTCTTGAGTACTGCTCC	197
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QY	198	TTGGACAAAACAATTCCGCTGTACTCGTTTACCTGACCTTTTACTGAACTGCAATCTTCCCA	257
Db	345	TTGGACAAAACAATTCCGCTGTACTCGTTTACCTGAACTGCAATCTTCCCA	404
QY	258	TTTGAAGTTTTCATACCTATGCTGTCCACCTGCTGTCTTCTCCCTTACAGACATATTTTG	317
Db	405	TTTGAAGTTTTCATACCTATGCTGTCCACCTGCTGTCTTCTCCCTTACAGACATATTTTG	464
QY	318	GCATCGTGTTTCAACAGATGTGTACCCAGCTGTCTCCATAGGAATTAACGAAAATGACAGATGCTG	377
Db	465	GCATCGTGTTTCAACAGATGTGTACCCAGCTGTCTCCATAGGAATTAACGAAAATGACAGATGCTG	524
QY	378	GCAGTGTATGGAACAAGCCCTAGTGTGGACGCCCTGTGAGGGTTTGTCCAGTTTCTCCAGACTCC	437
Db	525	GCAGTGTATGGAACAAGCCCTAGTGTGGACGCCCTGTGAGGGTTTGTCCAGTTTCTCCAGACTCC	584
QY	438	ACGCTGTTGGCATCAGGGGCGACGCTGTATGGAACCTGTGGTTTGTGTGAATGCAACGTCAATAC	497
Db	585	ACGCTGTTGGCATCAGGGGCGACGCTGTATGGAACCTGTGGTTTGTGTGAATGCAACGTCAATAC	644
QY	498	AAATTATATATGATGTGGTATGTTAAATAATGGCTCCCTGGGGGACATGACATTTTCTCCT	557
Db	645	AAATTATATATGATGTGGTATGTTAAATAATGGCTCCCTGGGGGACATGACATTTTCTCCT	704
QY	558	AATGGAAGCTCTCTTGTCTACTGCGCTCCATCTGTGGTATTTTAAACAGTGTGGATGATATAA	617
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Db	765	ATGAGGTGTCTGCATGATGTAAGTAAAGACATGATCTTGGAAATTAACCTGTGCGATTTTCT	824
QY	678	TCACAGCCAGTTTCTGATGAGAGAACAGAGTCTTCAGTTTTCATCTGCGCATCATGTGTGT	737
Db	825	TCACAGCCAGTTTCTGATGAGAGAACAGAGTCTTCAGTTTTCATCTGCGCATCATGTGTGT	884
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QY	785	-----	784
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QY	785	-----	784
Db	1005	GATGGCAGATGTAGTCTCAGGGCTCAGTGTGATATAGTCTGTATATATATATATAT	1064
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Db	1065	ACTGAGATATATCTTACACACTTACTAGCACACACAGGTATGTCAACAATTTGTGCTTTT	1124
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QY	785	-----ACGAAGCGCACAGAACTCAGCTGAAGCAATTTAC	821
Db	1185	TTTGCACCTGAAAACATTTTGCCAAAGCAAGGAGCAGAGAACATCTAGCTGAAACAATTTAC	1244
QY	822	GAAATTTGGTTCAGAGGAGGTGTCTCAACATGGGCTTTGTGACAAAGATTTTAAAGATCTT	881
Db	1245	GAAATTTGGTTCAGAGGAGGTGTCTCAACATGGGCTTTGTGACAAAGATTTTAAAGATCTT	1304
QY	882	GTTGTATATTTCAAGATGAATTAACATTTGATGGAAAAGAACTGTGAATCTTTTACAAAAGAA	941
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QY	942	AGTCTGGCTGATATTTTGAAAAATGAAATCTCTAGGACTGCGTAGTAAAGTGTGAGAAA	1001

Db	1365	AGTGTGGCTGATGATTTGAAAATTGGAATCTCTAGAGACTGGCGTAGTAAGTGTGAGAAA	1424
Qy	1002	ATTGAAGAGCTCAGAGCCAAAGTTAAATCCCTTTCTTCAGAAATTCCTGATGAATTTATA	1061
Db	1425	ATTGAAGAGCTCAGAGCCAAAGTTAAATCCCTTTCTTCAGAAATTCCTGATGAATTTATA	1484
Qy	1062	TGTCCCAATTACTAGAAACCTTAGAAAGATCCCGTCAATCCGATAGATATTCATAT	1121
Db	1485	TGTCCCAATTACTAGAAACCTTAGAAAGATCCCGTCAATCCGATAGATATTCATAT	1544
Qy	1122	GAAGAAGAACCAATGTAAAAATTGGATCAGCAAAAAAGAAACGTACAAATCCCATGACAAAT	1181
Db	1545	GAAGAAGAACCAATGTAAAAATTGGATCAGCAAAAAAGAAACGTACAAATCCCATGACAAAT	1604
Qy	1182	CTTGTTCTTCCTTCAGCGGTACTTACACCAATAGACTGTAAATGGCCATCAATAGA	1241
Db	1605	CTTGTTCTTCCTTCAGCGGTACTTACACCAATAGACTGTAAATGGCCATCAATAGA	1664
Qy	1242	TGCGTGGAGACACACCAAAAGTAAA	1266
Db	1665	TGCGTGGAGACACACCAAAAGTAAA	1689
RESULT 5			
LOCUS	AX748164	1811 bp	mRNA
DEFINITION	Sequence 1689 from Patent EPI308459.	linear	PAT 20-JUN-2003
ACCESSION	AX748164		
VERSION	AX748164.1	GI:32132552	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Isegai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hiro,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuko,Y.		
TITLE	Full-length cDNA sequences		
JOURNAL	Patent: BP 3308459-A 1689 07-MAY-2003;		
	Helix Research Institute (JP) ; Research Association for Biotechnology (JP)		
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Best Local Similarity 80.9%; Pred. No. 3,2e-230;			
Matches 1178; Conservative 0; Mismatches 3; Indels 276; Gaps 1.			
Qy	86	GGCTGTTTTCTTCAATAAAGAAACATGTGAACCTGATTCACACATTAGCTGATCATG	145
Db	125	GGCTGTTTTCTTCAATAAAGAAACATGTGAACCTGATTCACACATTAGCTGATCATG	184
Qy	146	TGAGGATGTCAACGTGCTGTGCTTCTCTTTCCCTCTTGAGTACTTGCTCTTGACAA	205
Db	185	TGAGGATGTCAACGTGCTGTGCTTCTCTTTCCCTCTTGAGTACTTGCTCTTGACAA	244
Qy	206	AACAATTGCGCTGACTCGTTACGTGACTTACTGAACGTGCACATTCCTCATTTGAAGTT	265
Db	245	AACAATTGCGCTGACTCGTTACGTGACTTACTGAACGTGCACATTCCTCATTTGAAGTT	304
Qy	266	TCATACCTATGCTGTCCAGTGTGCTGTCTTCTCCCTTCAGACATATTTTGGATCGTG	325
Db	305	TCATACCTATGCTGTCCAGTGTGCTGTCTTCTCCCTTCAGACATATTTTGGATCGTG	364
Qy	326	TTTCAACGATGTACCACTGTCTTATGGAATATCGAAAATGACAGATGCTGCGACATGAT	385

COMMENT

(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'- end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

Source

Location/Qualifiers

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CDS

Query Match 70.0%; Score 890.2; DB 9; Length 1811;
 Best Local Similarity 80.9%; Pred. No. 3.2e-230;
 Matches 1178; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

ORIGIN

86 GGCCTGTTTCTTCAATTAAGAACATGCTGAACCTGATTCACATTAAGTGAATCAG 145
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 125 GGCCTGTTTCTTCAATTAAGAACATGCTGAACCTGATTCACATTAAGTGAATCAG 184
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 206 AACAAATTCGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
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626 TCTGCATAGTGAAGAAACACATGATCTTGGAATTAACCTGCGGATTTTCTTCACAGCC 685
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 785 ----- 784
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RESULT 7

CQ491312 1996 bp DNA linear PAT 30-JAN-2004
 LOCUS CQ491312
 DEFINITION Sequence 23179 from Patent WO0160860.
 ACCESSION CQ491312
 VERSION CQ491312.1 GI:41456931
 KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Schlegel, R., Endege, W.O. and Monahan, J.E.
Gene differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 23179 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
Source
1. .1996
/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN
Query Match 69.1%; Score 878.8; DB 6; Length 1996;
Best Local Similarity 80.7%; Pred. No. 4e-227;
Matches 1166; Conservative 0; Mismatches 2; Indels 276; Gaps 1;
QY 99 CAAATAAAGAACATGCGAATCGATTCACACATTACTGATCGGTGACGATGTAC 158
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QY 159 TGGCTGCT 218
DB 64 TGGCTGCT 123
QY 219 TACTCGTTAGCTGATCTTACTGAACTGCACATCTCTCATTTGAAGTTTCATCTATGCT 278
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QY 279 GTCCACGCTGCTGCT 338
DB 184 GTCCACGCTGCTGCT 243
QY 339 ACCACTGCTCTATGGAATAGTAAATGAGACAGATGCTGACAGTGAACAGCTAGT 388
DB 244 ACCACTGCTCTATGGAATAGTAAATGAGACAGATGCTGACAGTGAACAGCTAGT 303
QY 399 GGCAGCCCTGTGAGGGTTTGGCAGTTTCCCGACATCTCACGTGTTGGCATCAGGGGCA 458
DB 304 GGCAGCCCTGTGAGGGTTTGGCAGTTTCCCGACATCTCACGTGTTGGCATCAGGGGCA 363
QY 459 GCTGATGGAACGTGGTTTGTGGATGCAACGATCAAAATATATATGATGGTGTAGT 518
DB 364 GCTGATGGAACGTGGTTTGTGGATGCAACGATCAAAATATATATGATGGTGTAGT 423
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DB 1444 TAAA 1447
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LOCUS CQ497179
DEFINITION Sequence 29046 from Patent WO0160860.
ACCESSION CQ497179
VERSION CQ497179.1 GI:41462815
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Schlegel, R., Endege, W.O. and Monahan, J.E.
Gene differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 29046 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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RESULT 10
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 ACCESSION BC061948
 VERSION BC061948.1 GI:38303926
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2130)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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 Generation and initial analysis of more than 15,000 full-length
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 JOURNAL MEDLINE 22388257
 PUBLISHED 12477932
 REFERENCE 2 (bases 1 to 2130)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (10-NOV-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabbs-rc@mail.nih.gov
 Tissue Procurement: Susan L. Sullivan, PhD.

FEATURES
 source
 CDNA Library Preparation: ResGen, Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
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 Galtherburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nih.gov
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PUBMED 12477932
REFERENCE 2 (bases 1 to 1547)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
cDNA Library Preparation: Michael Brownstein / Ted Ueda
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalley, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
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VERSION
AJ719461.1 GI:53127473
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Caldwell, R.B., Kierzek, A.M., Arakawa, H., Bezubov, Y., Zaim, J.,
Fiedler, P., Kutter, S., Blagoderaki, A., Kostovska, D., Koret, M.,
Plachy, J., Carminci, P., Hayashizaki, Y., and Buerstedde, J.M.
TITLE Full-length cDNAs from bursal lymphocytes to facilitate gene
function analysis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3818)
AUTHORS Caldwell, R.B.
TITLE Direct Submission


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LOCUS CO473162

DEFINITION Sequence 5029 from Patent WO0100860.

ACCESSION CO473162

VERSION CO473162.1 GI:41438781

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

AUTHORS Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Eucleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Schlegel, R., Endege, W.O. and Monahan, J.E.

Genes differentially expressed in human prostate cancer and their use

JOURNAL

Patent: WO 0160860-A 5029 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES

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ORIGIN

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Matches 365; Conservative 0; Mismatches 10; Indels 4; Gaps 2;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Title: US-10-077-111-13

Perfect score: 2047

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2031	99.2	1564	9	BC029520 Homo sapi
2	1984	96.9	1996	6	CQ491312 Sequence
3	1984	96.9	1996	6	CQ497179 Sequence
4	1978	96.6	1811	6	AX748164 Sequence

Result No.	Score	Query Match	Length	DB ID	Description
5	1978	96.6	1811	9	AK093494 Homo sapi
6	1978	96.6	1844	6	AR339277 Sequence
7	1978	96.6	1919	9	AK129983 Homo sapi
8	1823.5	89.1	1254	6	CQ728621 Sequence
9	1617	79.0	2130	10	BC061948 Homo sapi
10	1664	71.5	3818	5	AJ719461 Gallus ga
11	1373	67.1	1547	10	BC050792 Homo sapi
12	1236.5	59.9	1291	6	AX076675 Sequence
13	733	35.8	147021	2	AC006501 Homo sapi
14	731	35.7	145795	2	AC096419 Homo sapi
15	731	35.7	315463	2	AC122070 Homo sapi
16	728	35.6	177089	9	AC008277 Homo sapi
17	677	33.1	196403	2	AC102767 Homo sapi
18	677	33.1	209437	2	AC111119 Homo sapi
19	677	33.1	217352	10	AL929242 Mouse DNA
20	627.5	30.7	446	6	CQ473162 Sequence
21	626.5	30.6	409	6	CQ482331 Sequence
22	621.5	30.4	441	6	CQ503452 Sequence
23	621.5	30.4	441	6	CQ512287 Sequence
24	597	29.2	366	6	CQ096643 Sequence
25	597	29.2	366	6	CQ135438 Sequence
26	597	29.2	366	6	CQ218732 Sequence
27	597	29.2	366	6	CQ294537 Sequence
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30	532	26.0	297	6	CQ109842 Sequence
31	532	26.0	297	6	CQ148540 Sequence
32	532	26.0	297	6	CQ231810 Sequence
33	532	26.0	297	6	CQ307124 Sequence
34	532	26.0	297	6	CQ344013 Sequence
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36	311	15.2	153866	9	AC009307 Homo sapi
37	308.5	15.1	466	6	CQ097537 Sequence
38	308.5	15.1	466	6	CQ136375 Sequence
39	308.5	15.1	466	6	CQ213679 Sequence
40	308.5	15.1	466	6	CQ258151 Sequence
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43	300	14.7	180	6	CQ110706 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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clone MGC:33855 IMAGE:5301559), complete cds.
ACCESSION
BC029520
VERSION
BC029520.1 GI:20810486
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1564)
Serausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buelow,K.H., Schaefer,C.F., Shat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heileh,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,W.B., Bonaldo,N.F., Casavant,T.U.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodríguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 Schlegel, R., Endege, W.O. and Monahan, J.E.
 Genes differentially expressed in human prostate cancer and their
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 Patent: WO 0160860-A 29046 23-AUG-2001;
 Millennium Predictive Medicine, Inc. (US)
 Location/Qualifiers
 1. 1996
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 ORIGIN
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 Percent Similarity: 80.46% Conservative: 0
 Best Local Similarity: 80.46% Mismatches: 1
 Query Match: 96.92% Indels: 92
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 QY 41 AspPheThrGluLeuProHisSerProLeuIlePheHisThrTyrAlaValHisCysCys 60
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 ACCESSION AX748164
 VERSION AX748164.1 GI:32132552
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Seto, H., Ishii, S.,
 Yamamoto, J.I., Igono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
 Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and
 Masuko, Y.
 Full-length cDNA sequences
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 FEATURES
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Yama,M., Hata,H., Matanabe,M., Komatsu,T., Mizushima-Sugano,J.,
Sach,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,R.,
Nagao,T., Nomura,N., Kikuchi,H., Masuno,Y., Yamashita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

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PUBMED
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AUTHORS

TITLE

2
Ishibashi,T., Kanehori,K., Yosida,M., Matanabe,S., Ishida,S.,
Ono,Y., Horiuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
Kusano,Y., Matanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Makamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
Sekino,M., Kikuchi,H., Kanda,K., Magaruma,M., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahara,K., Masuno,Y., Nagai,K. and Isogai,T.
Unpublished
3 (bases 1 to 1811)
Isogai,T. and Yamamoto,J.
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7
Kazuo-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB) ; cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
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Evaluation; clone selection for full insert sequencing: HRI and
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ORIGIN

Alignment Scores:
Pred. No.: 6,13e-172 Length: 1811
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 9 Gaps: 1

US-10-077-111-13 (1-384) x AK093494 (1-1811)

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Db 210 TCCCTTTTCCCTCTGTGGCTACTGCTGCTCTGGACAAACAAATTCGCTGACTGTTACGT 269

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Db 270 GACTTACTGAACTGGACATCTTCATTTGAAGTTTCAATTAACCTTATGCTTCCACTGCTGC 329

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DEFINITION	Sequence 768 from patent US 6569662.				
ACCESSION	AR339277				
VERSION	AR339277.1	GI:33726134			

SOURCE

REFERENCE
AUTHORS
TITLE
JOURNAL

Unclassified.
1 (bases 1 to 1844)
Tang, Y.T., Zhou, P. and Drmanac, R.T.
Nucleic acids and polypeptides
Patient: US 6569662-A 768 27-MAY-2003

FEATURES

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Alignment Scores:	
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Best Local Similarity:	80.25%
Query Match:	96.63%
DB:	6
Gaps:	1
Length:	1844
Matches:	382
Conservative:	0
Mismatches:	2
Indels:	92

US-10-077-111-13 (1-384) X AR339277 (1-1844)

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OY	141	SeuLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
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OY	161	GlyAspLeuThrValITTPAspAspLysMecArgCysLeuHisSerGluLysAlaHisAsp	180
Db	644	GGTATATTAAACAGCTGGGATGATMAAATGAGGTGTGTGCATGATGMAAAGCACATGAT	703
OY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu	200
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OY	226	-----AlaArgArg	228
Db	1064	ATGCACAAACACAGTGAACATCTGGCAATTGACCTCGAAACACTTTGCCAACAGCAAGAGC	1122
OY	229	ThrGlnHisGlnLeuLysGlnPheThrGlnAspTrpSerGlnGluValIleSerThrTrp	248
Db	1124	ACAGAACATCAGCTGGAAGCAATTTACCGAAGATTGGTCTAGAGGAGAGATGTCTCAACATGG	1183
OY	249	LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly	268
Db	1184	CTTGTGTGCACAAAGATTMAAAGATCTGTGGTATTTTCAAGATGAATMAACATTGAATGGA	1243
OY	269	LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu	288
Db	1244	AAAGAACCTGTGAATCTTACAAAGAAAGTCTGGCTGATGATTTGGAAATTTGAATCTCTTA	1303
OY	289	GlyLeuAspSerLysValLeuArgLysIleGlnGlnLeuAspThrLysValLysSerLeu	308
Db	1304	GGACTCGGTAGTAATAAGTCTGAGGAAATTAAGAGGCTCAGAGCACCAAGTTAAATCCCTT	1363
OY	309	SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro	328
Db	1364	TCCTTCAGGAATTCCTGTGAATTAATATGTCCAATTACTAAGAACTTATTAAGAAATCCG	1423
OY	329	ValIleAlaSerAspGlyTrpSerTrpGlnLysGlnLysIleMetGlnAsnTrpIleSerLys	348
Db	1424	GTCATCGCATCAGATGGCTATTCTCATATCAAAAGAGAACGAATTTGATCAGCAAA	1483
OY	349	LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn	368
Db	1484	AAGAAACGTAACAAGTCCCATCACAACAATCTTGTTCTTCTTCAGGGGTATCTTACACCAAT	1543
OY	369	ArgThrLeuLysMetAlaIleAsnAspTrpLeuGlnThrHisGlnLys	384
Db	1544	AGGACTCTGAATAATGGCCATCAATAGATGGCTGGAGACACACCAAAAG	1591

RESULT 7

OY	121	ValValLeuTPpAnaIaGInserTfLyLeuThYrGcYsgIyservAlLysAspGly	140
Db	524	GTGGTTTTTGGAATGCACAGCTCATACAAATTAATATGATGGTAGTGTAAAGAATGC	583
OY	141	SeuLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	584	TCCTTGGGGGAGTAGTGATTTTCTCTATATGAAAGCTTCTTGTGCACGTGGCTCTCATGT	643
OY	161	GlyAspLeuThrValITTPAspAspLysMecArgCysLeuHisSerGluLysAlaHisAsp	180
Db	644	GGTATATTAAACAGCTGGGATGATMAAATGAGGTGTGTGCATGATGMAAAGCACATGAT	703
OY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu	200
Db	704	CTTGGAATATACCTGCTCGATTTTCTTCACAGCAGAGTTCTGATGGAGAACAGGCTTT	763
OY	201	GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer	220
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Db	824	TTTATCCCATATCTTAGGTTTGAAATTAAATATAAATGAACACTAGTGGGCACTGTGCT	883
OY	225	-----	225
Db	884	CTGTGTTGGCTTGCTGCTTTTCCCATGATGGGAGATGCTAGTCTCAGGGTCACTAGTAT	943
OY	225	-----	225
Db	944	AAGTCTGTCAATATATGATATCACTAATCTAGATAATACTTACACACTGACTACAGCAC	1003
OY	225	-----	225
Db	1004	ACCAGGATATGCACAACTTGCTTTTGACCTAATACCCTTTTACTTGCTACTGTTTCA	1063
OY	226	-----AlaArgArg	228
Db	1064	ATGCACAAACACAGTGAACATCTGGCAATTGACCTCGAAACACTTTGCCAAGCAAGAGAC	1122
OY	229	ThrGlnHisGlnLeuLysGlnPheThrGlnAspTrpSerGlnGluValIleSerThrTrp	248
Db	1124	ACAGAACATCAGCTGGAAGCAATTATACCGAATGTTGGTCAGAGGAGATGTCTCAACATGG	1183
OY	249	LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly	268
Db	1184	CTTGTGTGCACAAAGATTAAAGATCTGTGGTATTTTCAAGATGAATMAACATTGAATGGA	1243
OY	269	LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu	288
Db	1244	AAAGAACCTGTTGAATCTTACAAAGAAAGTCTGGCTGATGATTTGGAAATTTGAATCTCTTA	1303
OY	289	GlyLeuAspSerLysValLeuArgLysIleGlnGlnLeuAspArgThrLysValLysSerLeu	308
Db	1304	GGACTCGGTAGTAATAAGTCTGAGGAAATTAAGAGAGCTCAGAGCAAGAGTTAAATCCCTT	1363
OY	309	SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro	328
Db	1364	TCTTCAGGAATTCCTGTGAATTAATATGTCCAATTACTAAGAACTTATATAAAGATCCG	1423
OY	329	ValIleAlaSerAspGlyTrpSerTrpGlnLysGlnLysIleMetGlnAsnTrpIleSerLys	348
Db	1424	GTCATCGCATCAGATGGCTATTCTCATATCAAAAGAGAAAGAAATTTGATCAGCAAA	1483
OY	349	LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn	368
Db	1484	AAGAAACGTAACAAGTCCCATCACAACAATCTTGTTCTTCTTACGGGGTATCTTACACCAAT	1543
OY	369	ArgThrLeuLysMetAlaIleAsnAspTrpLeuGlnThrHisGlnLys	384
Db	1544	AGGACTCTGAATAATGGCCATCAATAGATGGCTGGAGACACACCAAAAG	1591

RESULT 7

LOCUS	AK129983	1919 bp	mRNA	linear	PRI 10-SEP-2003
DEFINITION	Homo sapiens cDNA FLJ26473 fis, clone KDN04521.				
ACCESSION	AK129983				
VERSION	AK129983.1	GI:34526702			
KEYWORDS	oligo capping; fis (full insert sequence).				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotic Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 Tachiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.				
TITLE	NEDO human cDNA sequencing project				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1919)				
AUTHORS	Sugano,S. and Suzuki,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (31-JUN-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)				
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.				
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	/db_xref="taxon:9606"				
	/clone="KDN04521"				
	/tissue_type="kidney"				
	/clone_lib="KDN"				
	/note="Cloning vector: pME18SFL3"				
ORIGIN					
Alignment Scores:					
Pred. No.:	6,62e-172	Length:	1919		
Score:	1978.00	Matches:	382		
Percent Similarity:	80.25%	Conservative:	0		
Best Local Similarity:	80.25%	Mismatches:	2		
Query Match:	96.63%	Indels:	92		
DB:	9	Gaps:	1		
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Db	318	TCTTTTCCCTTGGCTGCTACTTGGCTCTTGGACAAACAATTCGGCTTACCTGTTAGCT	377		
Qy	41	AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysGys	60		
Db	378	GACTTTACTGAACTGCCACATTTCTCAATGAAAGTTTCACTTAAGCTGCACGCTGC	437		
Qy	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80		
Db	438	TGTTTCTCCCTTCGACGACATTTTGTGCACTGCTTTCAACAGATGTGATCACTGTCTTA	497		
Qy	81	TTPAanthrgluanglycInMetLeuAlaValMetGluInProSerGlySerProVal	100		
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QY	101	ArgValCysGlnPheSerProAepSerThrCysLeuAlaSerGlyAlaIaAepGlyThr	120
Db	558	AGGGTTGGCCAGTITTTCCCGACTCCACGCGITTTGGCATCAGGGGCAAGCTGAAGAACT	617
QY	121	ValValLeuTPAAnaIaGlnSerCtyLysLeuTyraArgCysGlySerValLysAepGly	140
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QY	141	SerLeuAlaIaCysAlaPheSerProAenGlySerPhePheValThrGlySerSerCys	160
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QY	161	GlyAepLeuThrValTPAaPAsPlyMetArgCysLeuHisSerGlyLysValHisAaP	180
Db	738	GGTAAATTAACAGTGTGGAGATGAATAAATGAGGTCTGCATGATGAAAAGCAATCAT	797
QY	181	LeuGlyIleThrCysCysAaPheSerSerGlnProValSerAepGlyGlnGlnGlyLeu	200
Db	798	CTTGGAAATTAACCTGCTCGTGATTTTCTTTCACAGCGAGTTCTGATGAGAACAAAGCTT	857
QY	201	GlnPhePheArgLeuAlaSerCysGlyGlnAepCysGlnValLysIleTrpIleValSer	220
Db	858	CAGTTTTTCCACGCGCATCATGTGTCAGAGATTGGCCAAAGTCAAAATTTGCATTGTTCT	917
QY	221	PheThrHisIleLeu-----	225
Db	918	TTTACCCATATCTTAAGCTTTTGAATTAATAATATAAATGATACATGAGGGCACTGTGCT	977
QY	225	-----	225
Db	978	CCTGTTCTGGCTTGTGCTTTTCCCATGATGGCAGATGCTACTCAGAGTCACTGAT	1037
QY	225	-----	225
Db	1038	AAGTCTGATAGATATATGATATCAATAATCTGAGAAATTACTTTCACACATTGACTCAGAC	1097
QY	225	-----	225
Db	1098	ACCAAGTATGCACAACTGTGCTTTTGCACCTAATACCTTTACTGTTGCTACTGATTC	1157
QY	226	-----AlaArgArg	228
Db	1158	ATGACAAACACGTGAAATCATCTGGCAATTGACCTGGAAACATTTGCCAAGCAAGAGC	1217
QY	229	ThrGlnHisGlnLeuLysGlnPheThrGlnAspTrpSerGlnGluValIleSerThrTrp	248
Db	1218	ACAGAACTACGCTCGAAGCAATTTACCGAAGATTGGTCAAGAGAGATGTCTCAACTGG	1277
QY	249	LeuCysAlaGlnAaPLeuLysAaPLeuValGlyIlePheLysMetAraAsnIleAepGly	268
Db	1278	CTTGTGTGCACAAAGATTTAAAGATCTTGTGGTATTTTTCAGAGATTAACATTTGATGGA	1337
QY	269	LysGlnLeuLeuAaLeuThrLysGlnSerLeuAlaAaPLeuLysIleGlnSerLeu	288
Db	1338	AAAGAACTGTTGAATCTTACAAAAGAAAGCTGCTGATGATTTGAAATAATGAATCTTA	1397
QY	289	GlyLeuArgSerLysValLeuArgLysIleGlnGlnLeuArgThrLysValLysSerLeu	308
Db	1398	GGACTCGGTAGTAAGTGTCTGAGAAATTTGAAGAGCTCAGGACCAAGGTTAAATCCCTT	1457
QY	309	SerSerGlyIleProAepGlnPheIleCysAspProIleThrArgGlnLeuMetLysAaPPro	328
Db	1458	TCTTCAGAAATCTGTGATGAATTAATATGTCCAAATACTAAGAACTTAAGAAAGATCCG	1517
QY	329	ValIleAlaSerAepGlyTySerTyGlnLysGlnAlaMetGlnAsnTrpIleSerLys	348
Db	1518	GTCAATCGCATCAGATGGCTATTCATATGAAGAAAGCAATGAAAAATTTGGATCAGCAA	1577
QY	349	LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn	368
Db	1578	AAGAAAGCTAACAAATCCCATGACAAAACTTGTTCTTCCCTTCACGCGATACCTAACCAAA	1637

Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluTrpHisGlnLys 384
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RESULT 8
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 DEFINITION Sequence 15555 from Patent WO02068579.
 ACCESSION CQ729621
 VERSION CQ729621.1 GI:42301208

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
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 Patent: WO 02068579-A 15555 06-SEP-2002;
 PE Corporation (NY) (US)

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 source Location/Qualifiers
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 Pred. No.: 6,13e-158 Length: 1254
 Score: 1823.50 Matches: 357
 Percent Similarity: 85.95% Conservative: 4
 Best Local Similarity: 85.00% Mismatches: 20
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US-10-077-111-13 (1-384) x CQ729621 (1-1254)

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 VERSION BC061948.1 GI:38303926
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 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 2130)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heist, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheer, T.E., Brownstein, M.J., Uedin, T.B., Topchyan, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosack, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,


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Qy 368 AsnArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
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RESULT 11
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DEFINITION IMAGE:6742025), partial cds.
ACCESSION BC050792.1 GI:30048136
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 1547)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Mandy,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,K.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
Mckernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Rahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shewchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smalloe,D.E.,
Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
MEDLINE 12477932
REFERENCE
2 (bases 1 to 1547)
Strausberg,R.
Direct Submision
Submitted (09-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomes Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-3590,
USA
MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
cDNA Library Preparation: Michael Brownstein / Ted Usdin
laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Boedert, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hestao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candace McInerney, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saecodi, Jacquoline
Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranda Tasi, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov
Series: IRAL Plate: 46 Row: a Column: 6
This clone was selected for full length sequencing because it
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analysis.

FEATURES
Location/Qualifiers

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Query Match: 67.07% Indels: 104
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US-10-077-111-13 (1-384) x BC050792 (1-1547)

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DB 231 TCGGCTGCCCTCCGCGCACCTGCTCTTGSACAAGACATCCGCTGACTCCCTAAGT 290
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyAlaValHisCysCys 60
DB 291 GACTTCTCTGAACGCGGACTCCCGCTGAAGTTCACACCTAATGCTGCTCACTGCTGC 350
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThValLeu 80
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RESULT 12

AX077675

LOCUS

DEFINITION

AX077675

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sequence 130 from Patent WO0105970.

AX077675.1 GI:13122057

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 Yue, H., Tang, Y. T., Bandman, O., Hillman, J. L., Lai, P., Au-Young, J., Reddy, R., Yang, J., Baughn, M. R., Lu, D. A., Azimzai, Y. and Paterson, C.
TITLE
JOURNAL
Gcp-binding protein associated factors
Patent: WO 0105970-A 130 25-JAN-2001;
Incyte Genomics, Inc. (US)
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Location/Qualifiers
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Score: 1226.50 Matches: 246
Percent Similarity: 71.97% Conservative: 3
Best Local Similarity: 71.10% Mismatches: 4
Query Match: 59.92% Indels: 93
DB: 6 Gaps: 2

US-10-077-111-13 (1-384) x AX077675 (1-1291)

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DB 178 CAGCCAGTTTCTGATGAGAACAAAGCTTTCAGTTTTCAGATCGCATATGTGCTAG 237
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DB 238 GATTCGCAAGTCAAAATTGGATTGTTCTTTACCATATCTTAGGTTTGAATTA 297
QY 225 ----- 225
DB 298 TATATAAGTACACTGAGTGGGCACTGTCTCTGCTTCTGGCTTGTCTTTCCATGAT 357
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QY 225 ----- 225
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QY 225 ----- 225
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LOCUS Homo sapiens, clone hRPK.35_A_1, complete sequence.

DEFINITION
AC006501
VERSION
AC006501.5 GI:4309874
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
Homo sapiens, clone hRPK.35_A_1
1 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.

2 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckely, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Deyayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrester, C., Funke, R., Gage, D., Galagan, J., Gardy, S., Gilbert, D., Grant, G., Hages, B., Heathord, A., Horton, L., Howland, J. C., Jones, C., Kahn, L., Karatas, A., Lehoczeky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Nijhoff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Testaye, S., Toriella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, W.

Direct Submission
Submitted (03-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckely, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Deyayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrester, C., Funke, R., Gage, D., Galagan, J., Gardy, S., Gilbert, D., Grant, G., Hages, B., Heathord, A., Horton, L., Howland, J. C., Jones, C., Kahn, L., Karatas, A., Lehoczeky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Nijhoff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Testaye, S., Toriella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, W.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
Submitted (03-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckely, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Deyayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrester, C., Funke, R., Gage, D., Galagan, J., Gardy, S., Gilbert, D., Grant, G., Hages, B., Heathord, A., Horton, L., Howland, J. C., Jones, C., Kahn, L., Karatas, A., Lehoczeky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Nijhoff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Testaye, S., Toriella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, W.

Direct Submission
Submitted (03-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckely, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Deyayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrester, C., Funke, R., Gage, D., Galagan, J., Gardy, S., Gilbert, D., Grant, G., Hages, B., Heathord, A., Horton, L., Howland, J. C., Jones, C., Kahn, L., Karatas, A., Lehoczeky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Nijhoff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Testaye, S., Toriella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, W.

TITLE Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
JOURNAL Direct Submission
COMMENT Submitted (26-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 1, 1999 this sequence version replaced gi:4309777.
All repeats were identified using RepeatMasker: Smt, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

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TITLE	JOURNAL
REFERENCE	Unpublished
REFERENCE	2. (bases 1 to 245795)
AUTHORS	Worley, K.C.
JOURNAL	Direct Submission
	Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3. (bases 1 to 245795)
AUTHORS	Rat Genome Sequencing Consortium.
TITLE	Direct Submission
JOURNAL	Submitted (10-MAY-2003) Human Genome Sequencing Center, Department

On May 10, 2003 this sequence version replaced of:24819739. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/atl1/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GFNB
Center clone name: CH230-24D13
----- Summary Statistics

```

Consensus quality: 232948 bases at least Q40
Consensus quality: 234943 bases at least Q30
Consensus quality: 236332 bases at least Q20
Estimated insert size: 240759; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

- * NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
- * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter.
- * This sequence will be replaced
- * by the finished sequence as soon as it is available and the accession number will be preserved.
- * 1 245795: contig of 245795 bp in length.

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FEATURES
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/mol_type="genomic DNA"
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misc_feature
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/note="wgs_contig"

ORIGIN

Alignment Scores:
Pred. No.:      2.18e-54      Length:      245795
Score:          731.08       Matches:      164
Percent Similarity: 33.98%    Conservative: 10
Best Local Similarity: 32.03%  Mismatches:  20
Query Match:    35.71%      Indels:      318
DB:             2           Gaps:        1

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US-10-077-111-13 (1-384) X AC096419 (1-245795)

QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAlaAsnCysCysAlaPhe 20

Db 137442 ATGGTGAAGCTGATTCACACACTGGCGGATCACCGGTGATGACCTGCTGCGCCTTC 137383

21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysIrrIleArgLeuIyrSerLeuArg 40

DB 13/38Z 1CH1CMA9C1CC1BGCCAC1G1C1C11BGAUHA9ACCA1CCGCC1G1AC1CCC1AA91 13

[illegible]

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QY 121 ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyr----- 132

Db 137082 GTTGTTTGTGGAACGCACATTCATACAATAATATAGGTACGGCGGCTTAAACCTGCC 13

132	13
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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

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QY 132 ----- 13

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QY      132 -----
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QY      163 LeuThrValIrrPaSpApIySmcAryCyAlaLeuHIsersIuIySaIaHIsaPLeuGly 182
Db      136002 TTTCACAGCTGTGGATATGACAAATAGAGCTGTCTGCACAGCGAAGGACACAGACTCGGG 135943
QY      183 ILeThrCyAcCyAlaPheSerSergIInProValSer 194
Db      135942 ATCACCTGCTGCAGACTTTTCTCTCACAGCCCTCTCTCT 135907

RESULT 15
AC122070 315463 bp DNA linear HTG 19-NOV-2002
LOCUS Rattus norvegicus clone CH230-18218, *** SEQUENCING IN PROGRESS
DEFINITION **, 18 unordered pieces.
AC122070
AC122070.4 GI:25092709
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 315463)
Wuzny,D.,Marle, Metzker,M.,Lee, Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Albrooks,S., Amin,A., Anguiano,D.,
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Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
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Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,

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REFERENCE
AUTHORS Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
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Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Soza,J.,
Steinle,M., Strong,R., Sutton,A., Svarek,A., Tabor,P., Taylor,C.,
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Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,Y., Zhou,J., Zhou,X., Zhou,S., Dunn,D., von
Niederhuesern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G., and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 315463)
Worley,K.C.
Direct Submission
Submitted (22-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 315463)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23322130.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and unpaired
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

```

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----- Project Information
Center project name: GMBU
Center clone name: CH230-18218
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 246672 bases at least Q40
Consensus quality: 252029 bases at least Q30
Consensus quality: 255877 bases at least Q20
Estimated insert size: 247533; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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12613 12712: gap of unknown length
12713 45951: contig of 33239 bp in length
45952 46051: gap of unknown length
46052 50355: contig of 4304 bp in length
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286786 286885: gap of unknown length
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297396 298651: contig of 1257 bp in length
298652 298752: gap of unknown length
298753 300032: contig of 1181 bp in length
300033 300744: gap of unknown length
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310778 310877: gap of unknown length
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312535 312634: gap of unknown length
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Score: 731.00 Matches: 164
Percent Similarity: 33.98% Conservative: 10
Best Local Similarity: 32.03% Mismatches: 20
Query Match: 35.71% Indels: 318
DB: Gaps: 1
US-10-077-111-13 (1-384) x AC122070 (1-315463)
QY 1 MetValylsleuilehsthrleualaasphiglyaspaspvalancysysalape 20
Db 77249 ATGCTGAAAGCTGATTCACACACTGCGGATCAGCGTATGACCTCGCGCTTC
QY 21 SerPheSerleuamathrcysSerleuaspsthrilleargleuYrserleuarg 40
Db 77309 TCAATCCAGCTCTCGGCACCTGCTCTTGGACAGACCAATCCGCTGATCTCAAGT 77368
QY 41 AspPheThrGlubepProHisSerProleuLysPheHisThrTyralaValHisCysCys 60
Db 77369 GACTTTGCTGAACATGCCGACCTCCCGTTGAAGTTTACACAGTATGCCGTCCTGTC 77428
QY 61 CysPheSerProserglYhisilleleualaSerCysSerThrAspGlyThrValleu 80
Db 77429 AGCTTCTCGCGCTGAGACAGCTTTGGCGTCCGCTCGACAGACGCTACTACGCTACTG 77488
QY 81 TrpAsnThrGlubanglylmeleualaValMeGlubInProserglYserProval 100
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Db 77549 CGCGTTTCGCTCTTTCGCGGACTCCACTACTGSCATCAGGGGCTCGCATGGGCTCT 77608
QY 121 ValValleuThrAsnalaGlnSerTyrlYleuYr----- 132
Db 77609 GTTGTGTTGGAGAACGACATTCATCAAAATATATAGTAGCGCGCTTAAACCTGACC 77668
QY 132 ----- 132
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QY 132 ----- 132
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QY 132 ----- 132
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QY 132 ----- 132
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QY 132 ----- 132
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QY 133 ----- ArgCysGlySerValIysAspGlySerLeu 142
Db 78569 CTGAACCCCGGTCTGTCTGTTCTGTTTCAGGTGTGTGTGTCAAGGACAGCTCATTG 78628
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Db 78629 GTGGCCTGTGCGTTTCTCTCTGACGAGGCCCTCTGTGTCACTGCTCTCGGAGGGGAC 78688
QY 163 LeuThrValTyrPheAspLysMetArgCysLeuHisSerGluLysAlaHisAspLeuGly 182
Db 78689 TTGACAGTGTGGAGATGACAAATGAGGTGTCTGACACAGGAGGACACGACCTCGGG 78748
QY 183 IleThrCysAspPheSerSerGlnProValSer 194
Db 78749 ATCACCCTGCTGACGCTTTTCTCTCACAGCCTCTCTCT 78784
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Search completed: October 25, 2005, 03:22:25
Job time : 4011 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 04:07:29 ; Search time 519 Seconds
(without alignments)
14508.499 Million cell updates/sec

Title: US-10-077-111-12
Perfect score: 1272
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1272	100.0	1272	6	AAD45075 Human RET
2	977.2	76.8	1553	6	AAD45071 Human RET
3	965.8	75.9	1818	6	AAD45070 Human RET
4	964.2	75.8	1817	10	ADB47507 Human CDN
5	964.2	75.8	1844	4	AA158876 Human pol
6	964.2	75.8	1844	5	ADQ99098 DNA encod
7	964.2	75.8	1844	9	ADB48858 Novel hum
8	894	70.3	1773	8	AB224707 Human cel
9	890.2	70.0	1811	10	ADB63535 Human CDN
10	878.8	69.1	1996	5	ABV29028 Human pro
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12	877.8	69.0	1908	6	AAD45076 Human RET
13	867.8	68.2	1826	4	AA160662 Human pol
14	791	62.2	1623	4	AA164914 Beta-tran
15	782	61.5	1686	5	ADM19385 Novel hum
16	654	51.4	838	5	ADM19628 Novel hum
17	478.6	37.6	1291	4	AA58364 Human GTP
18	464	36.5	1901	6	AAD45073 Mouse RET
19	390	30.7	668	13	ADQ54461 Novel can
20	377.2	29.7	630	6	AAD45072 Human RET

C	21	335	26.3	446	5	ABV05038 Human pro
C	22	331.6	26.1	366	4	AA136816 Probe #55
C	23	331.6	26.1	366	4	AAK30903 Human bon
C	24	331.6	26.1	366	4	AAK05311 Human bra
C	25	331.6	26.1	366	4	AB30581 Human liv
C	26	331.6	26.1	366	6	AB305651 Human gen
C	27	329.8	25.9	409	5	ABV14207 Human pro
C	28	328.8	25.8	441	5	ABV43501 Human pro
C	29	328.8	25.8	441	5	ABV44135 Human pro
C	30	297	23.3	297	4	AA150015 Probe #18
C	31	297	23.3	297	4	AAK44005 Human bon
C	32	297	23.3	297	4	AAK18116 Human bra
C	33	297	23.3	297	4	AB343659 Human liv
C	34	297	23.3	297	6	AB318238 Human gen
C	35	291.6	22.9	419	3	AAH30188 Human col
C	36	179.6	14.1	466	4	ABA58107 Human foe
C	37	179.6	14.1	466	4	AA137710 Probe #63
C	38	179.6	14.1	466	4	AAK31840 Human bon
C	39	179.6	14.1	466	4	AAK06182 Human bra
C	40	179.6	14.1	466	4	AB331528 Human liv
C	41	179.6	14.1	466	6	AB306599 Human gen
C	42	176.8	13.9	180	4	ABA70710 Human foe
C	43	176.8	13.9	180	4	AA150879 Probe #19
C	44	176.8	13.9	180	4	AAK44908 Human bon
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ALIGNMENTS

RESULT 1	AAAD45075	AAAD45075 standard; DNA; 1272 BP.
ID	AAAD45075	standard; DNA; 1272 BP.
XX	AAAD45075;	
AC		
XX		
DT	27-DEC-2002	(first entry)
XX		
DE	Human RET16.2 splice variant DNA.	
XX		
KW	Human, RET16; intracellular signal; inflammation-related disease; asthma;	
KW	rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;	
KW	transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;	
KW	inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;	
KW	infective respiratory distress syndrome; cardiac; ulcerative colitis;	
KW	autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;	
KW	cellular migration disorder; cell proliferation disorder; calcification;	
KW	hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;	
KW	cardiovascular disease; Wegener's granulomatosis; atherosclerosis;	
KW	thalassemia; vasotropic; gene; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	111..1265
FT		/*tag= a
FT		/product= "Human RET16.2 splice variant protein"
XX		
XX	WO200266494-A2.	
XX	29-AUG-2002.	
XX	15-FEB-2002; 2002WO-US005162.	
XX	16-FEB-2001; 2001US-0269366P.	
XX	29-MAY-2001; 2001US-0294181P.	
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.	
XX	Toddard CG, Finger UN, Rillema J;	
XX	WPI; 2002-682760/73.	
XX	P-PSDB; AAE28167.	
DR		

XX New human, mouse or rat RET16 genes and proteins, involved in
PT intracellular signaling cascade, useful for in gene therapy, particularly
PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
PT tumors or neoplasms.
XX
PS Claim 1; Page 166; 175bp; English.
XX
CC The invention relates to human, mouse or rat RET16 genes and proteins,
CC involved in intracellular signaling cascade. The RET16 protein or
CC polynucleotide is useful for treating an inflammation-related disease or
CC disorder, e.g. Rheumatoid arthritis, juvenile arthritis, psoriasis,
CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
CC bowel disease, Crohn's disease, ulcerative colitis, inacute respiratory
CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
CC disease or disorder also includes disorders associated with aberrant
CC activation of the TNF-alpha pathway, disorders associated with aberrant
CC cellular migration, proliferation, metastasis, juvenile idiopathic
CC arthritis, haemogenous metastases of tumour cells, hyperinsulinaemia,
CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
CC tumour progression, Wegener's granulomatosis, stem cell transplantation
CC complications, ischaemia-reperfusion injury, thalassaemia, acute lung
CC injury, graft rejection, ischaemic heart, coronary artery calcification
CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
CC sequence is human RET16.2 splice variant DNA
XX

Sequence 1272 BP; 349 A; 269 C; 290 G; 364 T; 0 U; 0 Other;

Query Match 100.0%; Score 1272; DB 6; Length 1272;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAATTCGGCTTTTCACTCCGCGGACGTAACCCGACCCCGGCGCACTTGAAGCG 60
QY 61 GATCCCGCGCGCCGCTCTGAGAGCTGTTTTCTTCAAAATAAGAGTGAAC 120
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DB 421 AGTTTTCCAGACTCCAGCTGTTTGGCATCAGGGGAGCTGATGAACTGTGGT 480
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QY 601 CAGTGTGGATGATAAATAGAGTGTCTGCATGATGAAAAAGACATGATCTGAATTA 660
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QY 901 ATTAACATTTGATGAAAAAGAACTTTGATTTTCAAAAGAACTGCTGATGATTTGA 960
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QY 961 AAATTAATCTCTAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1020
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DB 1021 AGGTAAATCTCTTCTTCAAGAAATCTGATGATGATGATGATGATGATGATGAT 1080
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QY 1141 ATTGATCAGCAAAAGAAAGTACAGTCCCATGCAATCTTGTCTTCTTCAAGCG 1200
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QY 1201 TACTTACACCAATTAAGACTGTGAAATGAGCCATCAATGATGAGCTGAGACAC 1260
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QY 1261 AGTAAAGAAATTC 1272
DB 1261 AGTAAAGAAATTC 1272
RESULT 2
AAD45071
ID AAD45071 standard; DNA; 1553 BP.
XX
AC AAD45071;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human RET16 open reading frame (ORF) DNA.
XX
XX Human; RET16; intracellular signal; inflammation-related disease; asthma;
XX rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
XX transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
XX inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
XX inacute respiratory disease syndrome; cardiac; ulcerative colitis;
XX autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
XX cellular migration disorder; cell proliferation disorder; calcification;
XX hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
XX cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
XX thalassaemia; vasotropic; open reading frame; ORF; gene; ds.
XX
XX Homo sapiens.
XX

FH Key Location/Qualifiers
 FT CDS 3..1541
 FT /tag= a
 FT /product= "Human RET16 protein"
 FT /note= "CDS does not include start codon"
 FT /partial
 PN MO200266494-A2.
 XX
 XX 29-AUG-2002.
 XX
 XX 15-FEB-2002; 2002MO-US005162.
 XX PF
 XX 16-FEB-2001; 2001US-0269366P.
 PR 29-MAY-2001; 2001US-0294181P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX
 XX
 PI Todderud CG, Finger JN, Rillema J;
 XX
 XX WPI; 2002-682760/73.
 DR P-PSDB; AAE28164.
 XX
 PT New human, mouse or rat RET16 genes and proteins, involved in
 PT intracellular signaling cascade, useful for in gene therapy, particularly
 PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
 PT tumors or neoplasms.
 XX
 XX Claim 1; Page 150; 175pp; English.
 XX
 XX The invention relates to human, mouse or rat RET16 genes and proteins,
 CC involved in intracellular signaling cascade. The RET16 protein or
 CC polynucleotide is useful for treating an inflammation-related disease or
 CC disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
 CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
 CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
 CC bowel disease, Crohn's disease, ulcerative colitis, inacute respiratory
 CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
 CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
 CC disease or disorder also includes disorders associated with aberrant
 CC activation of the TNF-alpha pathway, disorders associated with aberrant
 CC cellular migration, proliferation, metastasis, juvenile idiopathic
 CC arthritis, haemogenous metastases of tumour cells, hyperinsulinaemia,
 CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
 CC tumour progression, Wegener's granulomatosis, stem cell transplantation
 CC complications, ischaemia-reperfusion injury, thalassemia, acute lung
 CC injury, graft rejection, ischaemic heart, coronary artery calcification
 CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
 CC sequence is human RET16 open reading frame (ORF) DNA
 XX
 XX Sequence 1553 BP; 428 A; 327 C; 348 G; 450 T; 0 U; 0 Other;
 Query Match 76.8%; Score 977.2; DB 6; Length 1553;
 Best Local Similarity 81.9%; Pred. No. 4.9e-288;
 Matches 1265; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

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 Qy 481 GGAATGACAGTATACCAATTATATGATGCTGATGTTAAAGATGCTCTGCGCG 540
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 Qy 541 CATGTGATTTTCTCCTAATGGAAGCTTCTTGTCACTGCTCCTCATGTTGATTTAA 600
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 Qy 785 ----- 784
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 Qy 785 -----AGCAGGCGCACAGACATC 804
 Db 1021 CAGTGAACATCTGGCAATTTGACCTGGAACACATTTGCCAAGCAAGCGCACAGAACATC 1080
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 Db 1081 AGCTGAAGCAATTTACCGAAGATTTGTCAGAGAGTGTCTCAACATGCTTGTGCAC 1140
 Qy 865 AAGATTTAAAGATCTTGTGTAATTTTCAAGATGAATTAACATGATGGAAGAAAGATGT 924
 Db 1141 AAGATTTAAAGATCTTGTGTAATTTTCAAGATGAATTAACATGATGGAAGAAAGATGT 1200
 Qy 925 TGAATCTTCAAAAGAAAGTGTGCTGATGATTTGAAAATTGAATCTCTAGAGCTGCTA 984
 Db 1201 TGAATCTTCAAAAGAAAGTGTGCTGATGATTTGAAAATTGAATCTCTAGAGCTGCTA 1260
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 Db 1261 GTAAGTGTGAGGAATTTGAAGAGCTCAGAGCAAGTGAATCCCTTCTTCAAGAA 1320
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Db 1321 TTCCTGATGATTATATATGTCATACTAGAGAACTTATGAAGAATCCGCTATCGCAT 1380
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QY 1165 CAGATGGCTATTTCATATGAAGAAGCATGAAAAATTGATGACGAAAAAGAACGTA 1224
Db 1441 CAGATGGCTATTTCATATGAAGAAGCATGAAAAATTGATGACGAAAAAGAACGTA 1500
QY 1225 AATGGCCATCAATAGATGGCTGGAGACACACCAAAAGTAAGA 1268
Db 1501 AATGGCCATCAATAGATGGCTGGAGACACACCAAAAGTAAGTA 1544

RESULT 3
AAD45070
ID AAD45070 standard; DNA; 1818 BP.
XX
AC AAD45070;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human RET16 DNA.
XX
DE Human; RET16; intracellular signal; inflammation-related disease; asthma;
KM rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
KM transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
KM inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
KM inactive respiratory distress syndrome; cardiac; ulcerative colitis;
KM autoimmune disease; cystic fibrosis; gene therapy; cyclostatic; neoplasm;
KM cellular migration disorder; cell proliferation disorder; calcification;
KM hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
KM cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
KM thalassemia; vasotropic; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 148..1578
FT /tag= a
FT /product= "Human RET16 protein"

MO200266494-A2.
29-AUG-2002.
15-FEB-2002; 2002MO-US005162.
16-FEB-2001; 2001US-0269366P.
PR 29-MAY-2001; 2001US-0294181P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PI Todderud CG, Finger JN, Rillema J;
DR MPI; 2002-682760/73.
DR P-PSDB; AAE28163.
XX
PT New human, mouse or rat RET16 genes and proteins, involved in
PT intracellular signaling cascade, useful for in gene therapy, particularly
PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
PT tumors or neoplasms.
XX
PS Claim 1; Page 147-148; 175pp; English.

The invention relates to human, mouse or rat RET16 genes and proteins,
CC involved in intracellular signaling cascade. The RET16 protein or
CC polynucleotide is useful for treating an inflammation-related disease or
CC disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
CC bowel disease, Crohn's disease, ulcerative colitis, inactive respiratory

CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
CC disease or disorder also includes disorders associated with aberrant
CC activation of the TNF-alpha pathway, disorders associated with aberrant
CC cellular migration, proliferation, metastasis, juvenile idiopathic
CC arthritis, haematogenous metastases of tumour cells, hyperinsulinaemia,
CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
CC tumour progression, Wegener's granulomatosis, stem cell transplantation
CC complications, ischaemia-reperfusion injury, thalassemia, acute lung
CC injury, graft rejection, ischaemic heart, coronary artery calcification
CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
CC sequence is human RET16 DNA
XX

SQ Sequence 1818 BP; 523 A; 373 C; 382 G; 540 T; 0 U; 0 Other;

Query Match 75.9%; Score 965.8; DB 6; Length 1818;

Best Local Similarity 81.8%; Pred. No. 1.7e-284;

Matches 1253; Conservative 0; Mismatches 2; Indels 276; Gaps 1;

QY 12 TCACCTGCGCGGACGTCGACCGCACCGCCGTGGGACCTTGAAGCGGATCCCGCG 71
Db 49 TCACCTGCGCGGACGTCGACCGCACCGCCGTGGGACCTTGAAGCGGATCCCGCG 108
QY 72 CCCCCCTCTCGACGCTGTTTTCTTCAATPAAGACATGGTGAACCTGATTCACACA 131
Db 109 CCCCCCTCTCGACGCTGTTTTCTTCAATPAAGACATGGTGAACCTGATTCACACA 168
QY 132 TTAGCGATCAGTGCATGACATGTCACCTGCTGCTTCCCTTTCCCTTGGCTACT 191
Db 169 TTAGCGATCAGTGCATGACATGTCACCTGCTGCTTCCCTTTCCCTTGGCTACT 228
QY 192 TGCTCCTTGACAAACAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
Db 229 TGCTCCTTGACAAACAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
QY 252 TCTCATGGAAGTTGATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
Db 289 TCTCATGGAAGTTGATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
QY 312 ATTTGGCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
Db 349 ATTTGGCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
QY 372 ATGCTGGCAGTGAAGACAGCTTATGTCAGGCTGTCAGGCTTCCAGTTTCCCA 431
Db 409 ATGCTGGCAGTGAAGACAGCTTATGTCAGGCTGTCAGGCTTCCAGTTTCCCA 468
QY 432 GACTCCAGCTGTTGGCATCAGGGGCACTGATGAACTGTGTTTGTGAAATGCACAG 491
Db 469 GACTCCAGCTGTTGGCATCAGGGGCACTGATGAACTGTGTTTGTGAAATGCACAG 528
QY 492 TCATCAAAATTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
Db 529 TCATCAAAATTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
QY 552 TCTCTTAATGAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
Db 589 TCTCTTAATGAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
QY 612 GATTAATGAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
Db 649 GATTAATGAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
QY 672 TTTTCTTCACAGCAGTTCTGATGAGAAAGCAAGCTTCAGTTTGTGACGCGCATCA 731
Db 709 TTTTCTTCACAGCAGTTCTGATGAGAAAGCAAGCTTCAGTTTGTGACGCGCATCA 768
QY 732 TGTGTGAGGATTCAGATCAAAATTTGATGTTCTTTTACCATACTT----- 784
Db 769 TGTGTGAGGATTCAGATCAAAATTTGATGTTCTTTTACCATACTTCTTAGGTTT 828
QY 785 ----- 784

```
Db      829 GAATTAATAATAAGTACAGTGGGCACTGCTCTCTGCTTGTGCTTGT 888
Qy      785 ----- 784
Db      889 TCCCATGATGGGAGATGCTAGTCTCAGGGTCAGTGGATTAAGTCTGTCAATGATATGAT 948
Qy      785 ----- 784
Db      949 ACTAATACTGAAATATACTTCAACATTTGACTGACACACAGTATATGTCACACTTGT 1008
Qy      785 ----- 784
Db      1009 GCTTTTGACCTATATACCTTTTACTTGTCTAGTGTCAATGACAAAGACATGACATC 1068
Qy      785 -----AGCAAGGGGACAGAACATCTCAGCTGAACCA 815
Db      1069 TGGCAATTTGACCTGGAAACATTTTGGCAAGGAGGACAGAAACATCTGAAACCA 1128
Qy      816 TTTACCGAAGATTGTCAGAGAGTGTCTCAACATGCTTTGTGACAAAGATTTTAAA 875
Db      1129 TTTACCGAAGATTGTCAGAGAGTGTCTCAACATGCTTTGTGACAAAGATTTTAAA 1188
Qy      876 GATCTTGTGTGATTTTCAAGATGATTAACATTTGATGAGAAAGAACTGTTGAATCTTACA 935
Db      1189 GATCTTGTGTGATTTTCAAGATGATTAACATTTGATGAGAAAGAACTGTTGAATCTTACA 1248
Qy      936 AAGAAAGCTGCTGATGATTTTGAAGAAATGATCTCTAGAGCTGCTTGAAGTCTG 995
Db      1249 AAGAAAGCTGCTGATGATTTTGAAGAAATGATCTCTAGAGCTGCTTGAAGTCTG 1308
Qy      996 AGGAAATTTGAAGAGCTCAGAGCAACAGTTAAATCCCTTTCTTCAAGAAATTCCTGATGA 1055
Db      1309 AGGAAATTTGAAGAGCTCAGAGCAACAGTTAAATCCCTTTCTTCAAGAAATTCCTGATGA 1368
Qy      1056 TTTATATGTCCTAATTAAGAGAACTTATGAAAGATCCGTCATCGCATGATGATGCTAT 1115
Db      1369 TTTATATGTCCTAATTAAGAGAACTTATGAAAGATCCGTCATCGCATGATGATGCTAT 1428
Qy      1116 TCATATGAAAGAGAGCAATGAGAAATTTGATTCAGCAAAAGAAAGAACTTCAAGTCCATG 1175
Db      1429 TCATATGAAAGAGAGCAATGAGAAATTTGATTCAGCAAAAGAAAGAACTTCAAGTCCATG 1488
Qy      1176 ACAAAATTTGCTCTTCTTCAAGGCTTACTTACACCAATAGAGTCTGAAATGGCCATC 1235
Db      1489 ACAAAATTTGCTCTTCTTCAAGGCTTACTTACACCAATAGAGTCTGAAATGGCCATC 1548
Qy      1236 AATAGATGCTGAGAGACACCAAAAGTAAA 1266
Db      1549 AATAGATGCTGAGAGACACCAAAAGTAAA 1579

RESULT 4
ADB47507 standard; cDNA; 1817 BP.
AC      ADB47507;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Human cDNA upregulated in dendritic cells SEQ ID NO 207.
XX
KM      ss; gene; human; dendritic cells; high throughput; cancer;
XX      infectious disease; autoimmune disease; allergy;
KM      graft versus host disease; vaccine enhancing; gene therapy.
XX
XX      Homo sapiens.
XX      OS
XX      US2003134283-A1.
XX      PN
XX      17-JUL-2003.
XX      PD
XX      03-OCT-2001; 2001US-00971392.
XX      PF
XX
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PR      03-OCT-2000; 2000US-0237652P.
XX
PA      (PETER/) PETERSON D P.
PA      (PEAR/) PEARSON C I.
PA      (COCK/) COCKS B G.
XX
PI      Peterson DP, Pearson CI, Cocks BG;
XX
DR      WPI; 2003-662509/62.
XX
XX      New combination comprises cDNAs that are differentially expressed in
PT      dendritic cells useful for preparing a composition for diagnosing or
PT      treating cancer, infectious disease, autoimmunity, allergy or graft
PT      versus host disease.
XX
PS      Claim 1; SEQ ID NO 207; 28pp; English.
XX
XX      The invention relates to a combination comprising cDNAs that are
CC      differentially expressed in dendritic cells (DC). Also included is a high
CC      throughput method for detecting differential expression of one or more
CC      cDNAs in a sample containing nucleic acids. The combination is useful for
CC      preparing a composition for diagnosing, treating and monitoring the
CC      treatment of cancer, infectious disease, autoimmunity, allergy or graft
CC      versus host disease, or for enhancing a vaccine. The present sequence
CC      represents a human cDNA upregulated in dendritic cells. Note: The
CC      sequence data for this patent did not form part of the printed
CC      specification but was obtained in electronic format directly from USPTO
CC      at seqdata.uspto.gov/sequence.html?docid=20030134283.
XX
SQ      Sequence 1817 BP; 519 A; 373 C; 383 G; 542 T; 0 U; 0 Other;
```

Query Match 75.8%; Score 964.2; DB 10; Length 1817;
Best Local Similarity 81.8%; Pred. NO. 5.2e-284;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

```
Qy      12 TCACCTGCGGCGGACGTGACCCGACCGCCGCTGGGACCTTGAAGCGGATCCGCGCG 71
Db      49 TCACCTGCGGCGGACGTGACCCGACCGCCGCTGGGACCTTGAAGCGGATCCGCGCG 108
Qy      72 CCCCCGCTCTGACAGCTGTTTTCTTCAATTAAGAACTGTGAACTGATTCACACA 131
Db      109 CCCCCGCTCTGACAGCTGTTTTCTTCAATTAAGAACTGTGAACTGATTCACACA 168
Qy      132 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
Db      169 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 228
Qy      192 TGCTCTTGAGCAAAACAATTCGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
Db      229 TGCTCTTGAGCAAAACAATTCGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
Qy      252 TCTTCATGAAAGTTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
Db      289 TCTTCATGAAAGTTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
Qy      312 ATTTTGCAATGCTGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
Db      349 ATTTTGCAATGCTGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
Qy      372 ATGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
Db      409 ATGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
Qy      432 GACTCCAGCTGTTTGGCATAGGGGACGCTGATGAACTGTGTTTGTGAAATGACAG 491
Db      469 GACTCCAGCTGTTTGGCATAGGGGACGCTGATGAACTGTGTTTGTGAAATGACAG 528
Qy      492 TCATACAAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
Db      529 TCATACAAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
Qy      552 TCTCTTAATGAAGCTTCTTGTCACTGCTCTGATGATGATGATGATGATGATGATGATGATGAT 611
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D 589 TCTCCTAATGGAAGCTTCTTTGTCACTGGCTCCTCATGTGATTTAAACAGTGGGAT 648
Q 612 GATTAATAAGGAGTGTGCACTAGTAAAAAGCAGATCTTGGAAATTCCTGCTGGAT 671
D 649 GATTAATAAGGAGTGTGCACTAGTAAAAAGCAGATCTTGGAAATTCCTGCTGGAT 708
Q 672 TTTTCTTCAAGCAGCTTTCTGTAGAGAAACAAGTCTTCAGTTTTTTCAGCTGGATCA 731
D 709 TTTTCTTCAAGCAGCTTTCTGTAGAGAAACAAGTCTTCAGTTTTTTCAGCTGGATCA 768
Q 732 TGTGTGACAGATTGCCAAGTCAAAATTTGGATTTCTTTTACCATATCTT----- 784
D 769 TGTGTGACAGATTGCCAAGTCAAAATTTGGATTTCTTTTACCATATCTTGGATTTT 828
Q 785 ----- 784
D 829 GAATTAATAATAAAGTACACTGAGTGGGCACTGTCTCTGCTGCTGCTTTT 888
Q 785 ----- 784
D 889 TCCCATGATGGGAGATGCTAGTCTCAGGGTCAAGTGAATTAAGTCTGTCAATATATGAT 948
Q 785 ----- 784
D 949 ACTAATAGTGAATATCTTACACATTGACTCAGACACACAGATATGTCAACAATTGT 1008
Q 785 ----- 784
D 1009 GCTTTGCACTTAATACCTTTTACTTGTCTGCTGTTCAATGACAAACAGTGAACATC 1068
Q 785 -----AGCAGGCGCAGACAGACATCAGTGAACAA 815
D 1069 TGGCAATTTGACCTGGAAACACTTTGCAAGCAAGGAGCAGACATCAGCTGAAGCAA 1128
Q 816 TTTTCCGAAGATTGTCAGAGAGAGTCTGTCAACATGCTTTGTGTGACAAAGTTTAAAA 875
D 1129 TTTTCCGAAGATTGTCAGAGAGAGTCTGTCAACATGCTTTGTGTGACAAAGTTTAAAA 1188
Q 876 GATCTGTTGGTATTTTTCAGATGATTAACATTGATGAAAGAAAGACTGTTGAATCTTACA 935
D 1189 GATCTGTTGGTATTTTTCAGATGATTAACATTGATGAAAGAAAGACTGTTGAATCTTACA 1248
Q 936 AAGAAAGTCTGCTGATGATTTGAAATTTGAAATCTTGAAGACTGCGTAAAGTCTG 995
D 1249 AAGAAAGTCTGCTGATGATTTGAAATTTGAAATCTTGAAGACTGCGTAAAGTCTG 1308
Q 996 AGGAAATTTGAAGAGCTCAGAGACCAAGTTAAATCCCTTTCTCAGGAATTCCTGATGAA 1055
D 1309 AGGAAATTTGAAGAGCTCAGAGACCAAGTTAAATCCCTTTCTCAGGAATTTCTGATGAA 1368
Q 1056 TTTATATGTCGAATTAAGAGAACTTAAGAAAGATCCGGTCAATCCGATCAGATGGCTAT 1115
D 1369 TTTATATGTCGAATTAAGAGAACTTAAGAAAGATCCGGTCAATCCGATCAGATGGCTAT 1428
Q 1116 TCATATGAAAAGAGCAATGGAATTTGGATCAGCAAAAAGAAACGTAACAGTCCCATG 1175
D 1429 TCATATGAAAAGAGCAATGGAATTTGGATCAGCAAAAAGAAACGTAACAGTCCCATG 1488
Q 1176 ACAAAATCTGTTCTTCTTCCAGGCGTACTTACACAAATTAAGGACTGTGAAAATGGGCATC 1235
D 1489 ACAAAATCTGTTCTTCTTCCAGGCGTACTTACACAAATTAAGGACTGTGAAAATGGGCATC 1548
Q 1236 AATAGATGGCTGGAGACACACCAAAAGTAAA 1266
D 1549 AATAGATGGCTGGAGACACACCAAAAGTAAA 1579

RESULT 5
AA158876
ID AA158876 standard; cdna; 1844 BP.
XX
AC
XX AA158876;
XX

DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1079.
XX
KW Human; nootropic; immunosuppressant; cytotactic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000MO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa,
PI Zhou P, Goodrich R, Dermanac RT,
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM39720.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Claim 1, SEQ ID NO 1079; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytotactic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other:
XX
Query Match 75.8%; Score 964.2; DB 4; Length 1844;
Best Local Similarity 81.8%; Pred. No. 5.2e-284;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;
Q 12 TCACCTGCGCGGACGCTGACCCGACCGCCGCTGGGACCTTGAAGCGCGATCCCGCGG 71
D 65 TCACCTGCGCGGACGCTGACCCGACCGCCGCTGGGACCTTGAAGCGCGATCCCGCGG 124
Q 72 CCCCCGCTCTGACAGCTGTTTTTTCTTCAATTAAGAAATGATGTAATTCATCACA 131
D 125 CCCCCGCTCTGACAGCTGTTTTTTCTTCAATTAAGAAATGATGTAATTCATCACA 184

Oy	132	TTAGCTGATCATGAGGAGAGATGTCACACGCTGAGCTTCTCTTTTCCCTCTTGGCTACT	191
Db	185	TTAGCTGATCATGAGGAGAGATGTCACACGCTGAGCTTCTCTTTTCCCTCTTGGCTACT	244
Oy	192	TGCTCTCTTGGA,CAAAACAATTCCGCTGTACTGTTACGTAAGTACTTACTGAACCTGGACAT	251
Db	245	TGCTCTCTTGGA,CAAAACAATTCCGCTGTACTGTTACGTAAGTACTTACTGAACCTGGACAT	304
Oy	252	TCTCCATTGAA,GTTCATACCTTAATGCTGTGCACTGCTGCTGTTTTCTCCCTTCAGAACAT	311
Db	305	TCTCCATTGAA,GTTCATACCTTAATGCTGTGCACTGCTGCTGTTTTCTCCCTTCAGAACAT	364
Oy	312	ATTTTGGCATGCTGTTCAACACAGATGCTACACTGTCTCTTAATGGAATACTGMAAATGACAG	371
Db	365	ATTTTGGCATGCTGTTCAACACAGATGCTACACTGTCTCTTAATGGAATACTGMAAATGACAG	424
Oy	372	ATGCTGGCAGTGGATGGAACAGCCTTAGTGGCAGCCCTGTGAGGGTTTGGCAGTTTTCGCCA	431
Db	425	ATGCTGGCAGTGGATGGAACAGCCTTAGTGGCAGCCCTGTGAGGGTTTGGCAGTTTTCGCCA	484
Oy	432	GACTCCACGTGTTTGGCATACAGGGCAGCTGATGGAACCTGTGGTTTTGTGAATGACAG	491
Db	485	GACTCCACGTGTTTGGCATACAGGGCAGCTGATGGAACCTGTGGTTTTGTGAATGACAG	544
Oy	492	TCATACAAATTAATATAGATGTGTGATGTGTTAAAGATGCTCTTGTGGCGGACGTGCATTT	551
Db	545	TCATACAAATTAATATAGATGTGTGATGTGTTAAAGATGCTCTTGTGGCGGACGTGCATTT	604
Oy	552	TCTCCTAATGGAAGCTTCTTTGTCACTGCTCCTCATGTGGATGTTTAA,CACTGAGGAT	611
Db	605	TCTCCTAATGGAAGCTTCTTTGTCACTGCTCCTCATGTGGATGTTTAA,CACTGAGGAT	664
Oy	612	GATAAAATGAGGTGTCTGCATAGTGA,AAAAGACATGATCTTTGGAATTAACCTGCTGCAT	671
Db	665	GATAAAATGAGGTGTCTGCATAGTGA,AAAAGACATGATCTTTGGAATTAACCTGCTGCAT	724
Oy	672	TTTTCTTCA,CA,CGCCAGTTTCTGTAGTGA,GAACAAAGTCTTCA,GTTTTTCGACTGGCATCA	731
Db	725	TTTTCTTCA,CA,CGCCAGTTTCTGTAGTGA,GAACAAAGTCTTCA,GTTTTTCGACTGGCATCA	784
Oy	732	TGTGTTCAAGATTTGGCAAGTCA,AAATTTTGGATTTGTTTCTTTAACCCATPATCTT-----	784
Db	785	TGTGTTCAAGATTTGGCAAGTCA,AAATTTTGGATTTGTTTCTTTAACCCATPATCTT-----	844
Oy	785	-----	784
Db	845	GAATTA,AAATAT,AAAAGTACACTGAGTGGGCACTGTGCTCTGTTCTGTGCTGTGCTTTT	904
Oy	785	-----	784
Db	905	TCCCATGATGGCAGATGCTAGTCTCAAGGTCAGTGAATAGTCTGTATATATATGAT	964
Oy	785	-----	784
Db	965	ACTAATACTGAGAATATACTTGCACATTTGACTGCAGCACACGAGTATGTCA,CAACTTGT	1022
Oy	785	-----	784
Db	1025	GCTTTTGCACCTAATATACCTTTTACTTCTACTGTGTTCAATGACAAAACAGTGAACATC	1082
Oy	785	-----AGCAAGGCGCACAGAACATCAGCTGAAGCA	815
Db	1085	TGGCAATTTGACCTGGAAACA,CTTTGCCAAGCAGAGAGCA,CAAGAACATCAGCTGAAGCA	1144
Oy	816	TTTACCAGGAATTTGTCAGAGAGTCTGTTCAACATGGCTTTTGTGCACAAAGTTTAAAA	875
Db	1145	TTTACCAGGAATTTGTCAGAGAGTCTGTTCAACATGGCTTTTGTGCACAAAGTTTAAAA	1202
Oy	876	GATCTTGTGTAATTTTCAAGATGGAATTA,CAATTTGAGAAAAAGACTGTTGATCTTACA	935
Db	1205	GATCTTGTGTAATTTTCAAGATGGAATTA,CAATTTGAGAAAAAGACTGTTGATCTTACA	1262
Oy	936	AAAGAAAGTCTTGCTGATGATTTGAAAATTTGAATCTTGA,CACTGCTGTGTAAGTCTGTG	995

Accession	Sequence	Position
Dp		
1265	AAAGAAAGCTGGCTGATGATTTGAAAATTGAATCTTAGAGCTGGCTAGTAAAGTCTG	1324
Qy	996	1055
Dp	1325	1384
Qy	1056	1115
Dp	1385	1444
Qy	1116	1175
Dp	1445	1504
Qy	1176	1235
Dp	1505	1564
Qy	1236	1266
Dp	1565	1595

RESULT 6
ADQ99098
ID ADQ99098 standard; cDNA; 1844 BP.
XX
AC ADQ99098;
XX
DT 23-SEP-2004 (first entry)
XX
DE DNA encoding human GPCR-like protein seqid 768.
XX
KM ophthalmological; immunomodulatory; cytostatic; antiatherosclerotic;
KM antiatherogenic; GPCR-like protein; ophthalmic disorder;
KM neurological disorder; immunological disorder; nephritic disorder;
KM hormonal dysfunction; cancer; atherosclerosis; diabetes;
KM molecular weight marker; food supplement; human; ss.
XX
OS Homo sapiens.
XX
PN US6569662-B1.
XX
PD 27-MAY-2003.
XX
PF 19-JUL-2000; 2000US-00620312.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Drmanac RT;
XX
DR WPI; 2001-442255/47.
XX
PT New G-protein-coupled receptor-like polypeptides and polynucleotides,
PT useful for treating diseases of ophthalmic, neurological, immunological
PT and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
PT and diabetes.
XX
PS Example 2; SEQ ID NO 768; 92pb; English.
XX
CC The invention describes an isolated polynucleotide (I) comprising a fully
CC defined (51) OF 749, 3188, 2464, 1169, 2936, 1467, 5773, 5714, 4041,
CC 1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as
CC given in the specification, its translated or protein coding portion, its
CC extracellular portion or its active domain. The GPCR-like polypeptides
CC and polynucleotides are useful for the treatment of diseases of
CC ophthalmic, neurological, immunological and nephritic systems. They may
CC also be used to treat normal dysfunction, cancer, atherosclerosis and
CC diabetes. The antibodies are useful for detecting or quantitating the

CC polypeptide in tissue. The polypeptides can also be used as molecular
 CC weight markers and as a food supplement. This sequence represents a human
 CC polynucleotide of the invention.

XX Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other;

Query Match 75.8%; Score 964.2; DB 5; Length 1844;
 Best Local Similarity 81.8%; Pred. No. 5.2e-284;
 Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

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QY 12 TCACCTGCGGGGACGTCGACCCGACCCCGGGGACCTTGAAGCGGATCCCGGCG 71
DB 65 TCACCTGCGGGGACGTCGACCCGACCCCGGGGACCTTGAAGCGGATCCCGGCG 124
QY 72 CCCCCGCTCTGCGAGCGTGTCTTCAATATAAGAACTGGGAACTGATTCACACA 131
DB 125 CCCCCGCTCTGCGAGCGTGTCTTCAATATAAGAACTGGGAACTGATTCACACA 184
QY 132 TTAGCTGATCAGTGAAGATGTCACCTGCTGCTTCTCTTCCCTTGGCTACT 191
DB 185 TTAGCTGATCAGTGAAGATGTCACCTGCTGCTTCTCTTCCCTTGGCTACT 244
QY 192 TGTCTCTTGGACAAACAAATTCGCTGACTGCTTACGTAGTGAATTTACTGAATGCCACAT 251
DB 245 TGTCTCTTGGACAAACAAATTCGCTGACTGCTTACGTAGTGAATTTACTGAATGCCACAT 304
QY 252 TCTCCATTGAAGTTTACATCTATGCTGCTGCTGCTGCTTCTCTTCCCTTGGACAT 311
DB 305 TCTCCATTGAAGTTTACATCTATGCTGCTGCTGCTGCTTCTCTTCCCTTGGACAT 364
QY 312 ATTTTGGCATGCTGTTCAACAGATGGTACCATGCTCTATGAAATCTGAAAATGACAG 371
DB 365 ATTTTGGCATGCTGTTCAACAGATGGTACCATGCTCTATGAAATCTGAAAATGACAG 424
QY 372 ATGCTGGCAGTGAAGAAAGCCTAGTGAAGAGCCCTGAGGTTTCCAGTTTCCCA 431
DB 425 ATGCTGGCAGTGAAGAAAGCCTAGTGAAGAGCCCTGAGGTTTCCAGTTTCCCA 484
QY 432 GACTCCACGTTTGGCATCAGGGGACGTCGATGAAACTGTGGTTTGTGGAATGACAG 491
DB 485 GACTCCACGTTTGGCATCAGGGGACGTCGATGAAACTGTGGTTTGTGGAATGACAG 544
QY 492 TCATCAAAATTATATAGATGTGTAGTGTAAAGATGGCTCTTGGCGGAGTGCATTT 551
DB 545 TCATCAAAATTATATAGATGTGTAGTGTAAAGATGGCTCTTGGCGGAGTGCATTT 604
QY 552 TCTCCCTAAATGAGAGCTCTTGTTCACCTGCTCTCATATGATGTAATTAAGATGGAGAT 611
DB 605 TCTCCCTAAATGAGAGCTCTTGTTCACCTGCTCTCATATGATGTAATTAAGATGGAGAT 664
QY 612 GATAAATGAGAGTGTCTGATAGTGAATAAGACATGATCTTGAATTAACCTGTCGAT 671
DB 665 GATAAATGAGAGTGTCTGATAGTGAATAAGACATGATCTTGAATTAACCTGTCGAT 724
QY 672 TTTTCTTACAGCCAGTTTCTGATGAGAAAGAGTCTTCAAGTTTTCAGATGGCATCA 731
DB 725 TTTTCTTACAGCCAGTTTCTGATGAGAAAGAGTCTTCAAGTTTTCAGATGGCATCA 784
QY 732 TGTGGTCAGAGTGGCAAGTCAAAATTTGGATGTTTCCCTTACCAATATCTT----- 784
DB 785 TGTGGTCAGAGTGGCAAGTCAAAATTTGGATGTTTCCCTTACCAATATCTTAAGTTT 844
QY 785 ----- 784
DB 845 GAATTAATAATATAAAGTACACTGAGTGGGACCTGTGCTCTGTCTGAGCTTGTGCTTT 904
QY 785 ----- 784
DB 905 TCCCATGATGGGACAGATGCTAGTCTCAGGGTCAGTGAATAGTCTGTCAATATATGAT 964
QY 785 ----- 784
DB 965 ACTAATATGAGAAATATCTTCAACACTTGTACAGACACCAAGTATGTCACAACTTGT 1024

```

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QY 785 ----- 784
DB 1025 GCTTTTGCACTAATACCTTTTACTGTCTGTTCAATGACAAAAAGTGAACATC 1084
QY 785 -----AGCAAGCGCACAGAACATGAGTGAACAA 815
DB 1085 TGGCAATTTGACCTGGAAACATTTGCCAAGCAAGGACACAGAACATCAGCTGAAGCAA 1144
QY 816 TTTTACCGAAGATTGGTCAGAGAGGTCGCTCAACATGCTTTGTGACAAAGTTTAAAA 875
DB 1145 TTTTACCGAAGATTGGTCAGAGAGGTCGCTCAACATGCTTTGTGACAAAGTTTAAAA 1204
QY 876 GATCTGTGTGATTTTCAAGATGAATTAACATTTAGTGAAGAAAGAACTGTGAATCTTACA 935
DB 1205 GATCTGTGTGATTTTCAAGATGAATTAACATTTAGTGAAGAAAGAACTGTGAATCTTACA 1264
QY 936 AAGAAAGTCTGCTGATGATTTGAAAATGGAATCTTAGGACTGCGTAAAGTGTG 995
DB 1265 AAGAAAGTCTGCTGATGATTTGAAAATGGAATCTTAGGACTGCGTAAAGTGTG 1324
QY 996 AAGAAATTTGAAGAGCTCAGACCAAGTTAAATCCCTTCTTCAAGAAATTCCTGATGAA 1055
DB 1325 AAGAAATTTGAAGAGCTCAGACCAAGTTAAATCCCTTCTTCAAGAAATTCCTGATGAA 1384
QY 1056 TTTATATGTCAAATACTAGAGAACTTATGAAAGATCCGTCATGCGATCAGATGGCTAT 1115
DB 1385 TTTATATGTCAAATACTAGAGAACTTATGAAAGATCCGTCATGCGATCAGATGGCTAT 1444
QY 1116 TCATATGAAAAGGAACTGAAAAATTGGATCAGCAAAAAGAAAGTCAAGTCCCATG 1175
DB 1445 TCATATGAAAAGGAACTGAAAAATTGGATCAGCAAAAAGAAAGTCAAGTCCCATG 1504
QY 1176 ACAATCTTGTCTTCTTCAAGCGTACTTACACCAAATAGGACTGTGAAAATGGCATTC 1235
DB 1505 ACAATCTTGTCTTCTTCAAGCGTACTTACACCAAATAGGACTGTGAAAATGGCATTC 1564
QY 1236 AATAGATGCTGAGACACACCAAAAAGTAAA 1266
DB 1565 AATAGATGCTGAGACACACCAAAAAGTAAA 1595

RESULT 7
ADB48858
ID ADB48858 standard; cDNA; 1844 BP.
XX
AC ADB48858;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA SEQ ID NO 768.
XX
KW ss; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
PN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PF 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIU/) LIU C.
PA (ASUNDI/) ASUNDI V.
PA (DRMANAC/) DRMANAC R T.
XX
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;

```


XX MPI; 2003-678194/64.
 XX DR New polynucleotide, useful for treating diseases e.g., cancer or
 PT neurodegenerative diseases.
 XX PS Claim 1; SEQ ID NO 768; 99p; English.
 XX CC The invention relates to a polynucleotide comprising a sequence given in
 CC the specification, or its mature protein-coding portion, or its
 CC complement. The polynucleotide is useful for treating diseases e.g.,
 CC cancer or neurodegenerative diseases and many others listed in the
 CC specification. The present sequence represents a novel human cDNA. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPRO
 CC at seqdata.uspro.gov/sequence.html?docID=20030104529.
 SX Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other;
 QY Query Match 75.8%; Score 964.2; DB 9; Length 1844;
 Best Local Similarity 81.8%; Pred. No. 5.2e-284;
 Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

12 TCACTGCGGCGACGTGACCCGACCGCCGTGGGACCTTGAAGCGGATCCCGCG 71
 65 TCACTGCGGCGACGTGACCCGACCGCCGTGGGACCTTGAAGCGGATCCCGCG 124
 72 CCCCCCTCTCGACGCTGTTTTCTTCAATAAAGACATGTAAGATTCACACA 131
 125 CCCCCCTCTCGACGCTGTTTTCTTCAATAAAGACATGTAAGATTCACACA 184
 132 TTAGCTGATGATGGTGAAGATGTCACCTGCTGCTCTTCCCTTCCCTGGCTACT 191
 185 TTAGCTGATGATGGTGAAGATGTCACCTGCTGCTCTTCCCTTCCCTGGCTACT 244
 192 TGGCTCTTGGACAAACAAATTCGCTGCTACTGCTTACGTGACCTTACGTGACCA 251
 245 TGGCTCTTGGACAAACAAATTCGCTGCTACTGCTTACGTGACCTTACGTGACCA 304
 252 TGTTCATGTAAGTTCTTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
 305 TGTTCATGTAAGTTCTTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
 312 ATTTGGCATCGTGTAAACAGATGTAACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
 365 ATTTGGCATCGTGTAAACAGATGTAACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
 372 ATGCTGCAATGATGTAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
 425 ATGCTGCAATGATGTAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
 432 GACTCCACGTTGTTGGCATGAGGGGACGCTGATGAACTGTTGTTGTAATGACAG 491
 485 GACTCCACGTTGTTGGCATGAGGGGACGCTGATGAACTGTTGTTGTAATGACAG 544
 492 TCAATCAAAATTAATTAATGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 551
 545 TCAATCAAAATTAATTAATGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 604
 552 TCTCTTAATGGAAGCTTCTTTGCTACGCTGCTCTCATGTTGTTGTTAAAGTGGGAT 611
 605 TCTCTTAATGGAAGCTTCTTTGCTACGCTGCTCTCATGTTGTTGTTAAAGTGGGAT 664
 612 GATTAATGAGGTGTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 671
 665 GATTAATGAGGTGTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 724
 672 TTTTCTTCAAGCAGTTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 731
 725 TTTTCTTCAAGCAGTTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 784
 732 TGTGTCAGGATTCGCAAGTCMAAATTTGATTTCTTTTACCAATCTT----- 784

DB 785 TGTGTCAGGATTCGCAAGTCMAAATTTGATTTCTTTTACCAATCTTAGTTTT 844
 QY 785 ----- 784
 DB 845 GAATTAATAATTAATAAGTACAGTGGGACTGTCTGCTGCTGCTGCTTTT 904
 QY 785 ----- 784
 DB 905 TCCCATGATGGGAGATGCTAGTCTCAGGTCAGTGATTAAGTCTGATATATGAT 964
 QY 785 ----- 784
 DB 965 ACTAATAGTGAATATCTTACACATGACTGACAGACACAGATGTCACAACTTGT 1024
 QY 785 ----- 784
 DB 1025 GCTTTTGACCTAATACCTTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
 QY 785 -----AGCAAGGCGACAGAACATCTAGTGAAGCAA 815
 DB 1085 TGGCAATTTGACCTGGAACACCTTTGCGCAAGCAAGGACAGACATCTAGCTGAAGCAA 1144
 QY 816 TTACCGAAGATTTGCTCAGAGAGTCTCTCAACATGCTTTGTGCAAGAATTTAAAA 875
 DB 1145 TTACCGAAGATTTGCTCAGAGAGTCTCTCAACATGCTTTGTGCAAGAATTTAAAA 1204
 QY 876 GATCTTGTGTTTCTTCAAGATGAAATTAATGATGTAAGTAAAGTAAAGTAAAGTAA 935
 DB 1205 GATCTTGTGTTTCTTCAAGATGAAATTAATGATGTAAGTAAAGTAAAGTAAAGTAA 1264
 QY 936 AAAGAAAGTCTGCTGATGATTTGAAATTTGAATCTCTAGAGTCTGCTGATTAAGTCTG 995
 DB 1265 AAAGAAAGTCTGCTGATGATTTGAAATTTGAATCTCTAGAGTCTGCTGATTAAGTCTG 1324
 QY 996 AGGAAATTTGAAGAGCTCAGAGCAAGTTAAATCCCTTTCTTCAAGAAATTCCTGATGAA 1055
 DB 1325 AGGAAATTTGAAGAGCTCAGAGCAAGTTAAATCCCTTTCTTCAAGAAATTCCTGATGAA 1384
 QY 1056 TTTATATGTCATTAATTAAGAACTTAAGAAAGTCCGCTCATCGATCGATGCTAT 1115
 DB 1385 TTTATATGTCATTAATTAAGAACTTAAGAAAGTCCGCTCATCGATCGATGCTAT 1444
 QY 1116 TCAATGAAAGAGCAATGAAATTTGGATGAGCAAAAGAAAGTAAAGTAAAGTAAAGTAA 1175
 DB 1445 TCAATGAAAGAGCAATGAAATTTGGATGAGCAAAAGAAAGTAAAGTAAAGTAAAGTAA 1504
 QY 1176 ACAATCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1235
 DB 1505 ACAATCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1564
 QY 1236 AATGATGCTGAGACACACCAAAAGTAA 1266
 DB 1565 AATGATGCTGAGACACACCAAAAGTAA 1595

RESULT 8
 AB224707
 ID AB224707 standard; cDNA; 1773 BP.
 XX
 AC AB224707;
 XX
 DT 07-Apr-2003 (first entry)
 XX
 DE Human cell growth, differentiation and death protein CGPD-19 cDNA.
 XX
 KW CGPD-19; cell growth; cell differentiation; cell death; human;
 KW cytosolic; antiarteriosclerotic; hepatotropic; antiinflammatory;
 KW antiparasitic; antianemic; ophthalmological; auditory; anticonvulsant;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW neuroleptic; tranquilizer; immunosuppressive; anti-HIV; antiallergic;
 KW antidiabetic; antihypertensive; dermatological; nephrotoxic;
 KW antineumatic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 KW antineumatic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 KW antineumatic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;

Db	785	CCAAAGTCAAAATTTGGATTGTTCTTTTACCCATATCTTAGGTTTGAATTAATAATTA	844
QY	785	-----	784
Db	845	AAGTAACTAGTGGGCACGTGGCTCCTGTTCTGGCTTGCTTTTCCATGATGGGCA	904
QY	785	-----	784
Db	905	GATGCTACTCTCAGGGTCATGGATTAAGTCTGTCTATAGTATATGATACTAATTA	964
QY	785	-----	784
Db	965	TATACCTTCAACATTTGACTCAGCACACCAAGGTATGTCAAACTTGCTGTTTGCA	1024
QY	785	-----	784
Db	1025	TACCTTTTACTTGCTACTGTTCTCAATGGACAAAACAGTGAACATCTGGCAATTTG	1084
QY	785	-----AGCAAGCGCACAGAAATATCAGCTGAAGCAATTTACCGAAGATTG	829
Db	1085	GGAAACACTTTTGCCACGACGAAGAGACAGAACATCAGCTGAAGCAATTTACCGA	1144
QY	830	GTCAGAGAGGTGCTCTCAACATGGCTTTGTGCACAGATTTAAAGATCTTGTTGG	889
Db	1145	GTCAGAGAGAGATGCTCAGATGGCTTTGTGCACAGATTTAAAGATCTTGTTGGAT	1204
QY	890	TTTCAAGATGATATACTTTGATGGAAAAGACTGTTGAATCTTACAAAGAAAGCTGG	949
Db	1205	TTTCAAGATGATATACATTTGATGGAAAAGACTGTTGAATCTTACAAAGAAAGCTGG	1264
QY	950	TGATGATTTGAAAATTTGAATCTCTAGACCTGCTAGTAAGTGTGAGAAAATTTGA	1009
Db	1265	TGATGATTTGAAAATTTGAATCTCTAGACCTGCTAGTAAGTGTGAGAAAATTTGA	1324
QY	1010	GCTCAGAGCCAAAGTTAAATCCCTTTCTTCAGGAATCTCTGATGAATTTATGTCCA	1069
Db	1325	GCTCAGAGCCAAAGTTAAATCCCTTTCTTCAGGAATCTCTGATGAATTTATGTCCA	1384
QY	1070	AACCTAGAGAACTTATGAAGAATCCGGTCATGGCATCAGATGGCTATTCATATGAAA	1129
Db	1385	AACCTAGAGAACTTATGAAGAATCCGGTCATGGCATCAGATGGCTATTCATATGAAA	1444
QY	1130	AGCAATGGAAAATTTGATCAGCAAAAAGAAAGTACAGTCCCATGACAAATCTTGTTCT	1189
Db	1445	AGCAATGGAAAATTTGATCAGCAAAAAGAAAGTACAGTCCCATGACAAATCTTGTTCT	1504
QY	1190	TCTCTTACGGGTACTTACACCAAAATAGGACTCTGAAAATGGCCATCAATAGATGGCTGA	1249
Db	1505	TCTCTTACGGGTACTTACACCAAAATAGGACTCTGAAAATGGCCATCAATAGATGGCTGA	1564
QY	1250	GACACACCCAAAAGTTAA 1266	
Db	1565	GACACACCCAAAAGTTAA 1581	

RESULT 10
ABV29028
ID ABV29028 standard; cDNA; 1996 BP.

DT	16-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker cDNA 29019.

KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker.
KW	pharmacogenomic marker; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200160860-A2.
XX	

[illegible]

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OY 579 GGCCTCCTATGCTGATTTTAACAGTGGATGATAAATAGAGTGTCTGCATAGTGA 638
DB 484 GGCTTCCTATGATGGATTTTAACAGTGGATGATAAATAGAGTGTCTGCATAGTGA 543
OY 639 AAGACATGATCTTGGAAATTAACAGTGGATGATAAATAGAGTGTCTGCATAGTGA 698
DB 544 AAGACATGATCTTGGAAATTAACAGTGGATGATAAATAGAGTGTCTGCATAGTGA 603
OY 699 GAACAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 758
DB 604 GAACAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 663
OY 759 TGATTTGTTCTTTTACCATATCTT 784
DB 664 TGATTTGTTCTTTTACCATATCTT 723
OY 785 784
DB 724 GGGCAGTGTGCTCTGTTGCTTGGCTTTTCCCATGATGGGAGATGCTAGTCTCA 783
OY 785 784
DB 784 GGGTCACTGATGAAGTCTGATAGTATAGTATCTAATAGTGAATATATCTTACAGACA 843
OY 785 784
DB 844 TTGACTACGACACACAGATATGTCACAACTTGTCTTTTGACACTTAATACCTTTTACTT 903
OY 785 784
DB 904 GCTACTGTTCAATGACAAACAGTGAACATCTGGCAATTTGACCTGGAACACTTTGC 963
OY 785 --AGCAAGGCGCAGACAAATCATCAGTGAAGCAATTTACCAAGATTTGCTCAGAGAGTCTC 842
DB 964 CAAGCAAGGCGCAGACAAATCATCAGTGAAGCAATTTACCAAGATTTGCTCAGAGAGAT 1023
OY 843 GTCTCAACATGCGCTTTGCGACAGATTTTAAGATCTTGTGATTTTCAAGATGAAT 902
DB 1024 GTCTCAACATGCGCTTTGCGACAGATTTTAAGATCTTGTGATTTTCAAGATGAAT 1083
OY 903 AACATGATGGAAGAAAGAACTGTTGAATCTTACAAAGAAAGTCTGCTGATGATTTGAA 962
DB 1084 AACATGATGGAAGAAAGAACTGTTGAATCTTACAAAGAAAGTCTGCTGATGATTTGAA 1143
OY 963 ATTGAATCTTGAAGTCTGCTGATGATTTGAAAGTCTGAGAACTCAGACCAAG 1022
DB 1144 ATTGAATCTTGAAGTCTGCTGATGATTTGAAAGTCTGAGAACTCAGACCAAG 1203
OY 1023 GTTAAATCCCTTTCTTCAAGAAATCTGATGAATTTATGTCGAATTAACATAGAGACTT 1082
DB 1204 GTTAAATCCCTTTCTTCAAGAAATCTGATGAATTTATGTCGAATTAACATAGAGACTT 1263
OY 1083 ATGAAGATCCGTCATCGATCGATGATGCTATTCATATGAAGAAAGCAATGAAAT 1142
DB 1264 ATGAAGATCCGTCATCGATCGATGATGCTATTCATATGAAGAAAGCAATGAAAT 1323
OY 1143 TGATTCAGCAAAAGAAAGTCAAGTCCATGCAAAATCTTGTCTTCTTCAAGCGTA 1202
DB 1324 TGATTCAGCAAAAGAAAGTCAAGTCCATGCAAAATCTTGTCTTCTTCAAGCGTA 1383
OY 1203 CTTACACCAATATGAGATCTGGAAGTCCATGCAATGATGAGTGGAGACACACCAAG 1262
DB 1384 CTTACACCAATATGAGATCTGGAAGTCCATGCAATGATGAGTGGAGACACACCAAG 1443
OY 1263 TAAA 1266
DB 1444 TAAA 1447
```

RESULT 11
ABV23190
ID ABV23190 standard; cDNA; 1996 BP.

```
XX AC ABV23190:
XX XX
XX 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 23181.
XX KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX FN W0200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-018319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PT Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PT Claim 1; Page 4166-4167; 11750pp; English.
XX XX
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX XX
SQ Sequence 1996 BP; 615 A; 378 C; 447 G; 543 T; 0 U; 13 Other:
Query Match 69.1%; Score 878.8; DB 5; Length 1996;
Best Local Similarity 80.7%; Pred. No. 7.9e-258;
Matches 1166; Conservative 0; Mismatches 2; Indels 276; Gaps 1.
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|||||
244 ACCACTGCTCTATGGAATACTGAAAAATGACAGATGCTGGCAGTGAATGAAAGCCCTAGT 303
QY 399 GGGAGCCCTGTGAGGGTGTGGCCAGTTTCCCGAGACTCCACGCTGTTGGATCAGGGGCA 458
Db 304 GGGAGCCCTGTGAGGGTGTGGCCAGTTTCCCGAGACTCCACGCTGTTGGATCAGGGGCA 363
QY 459 GCTGATGAACTGTGGTGTGTGGAAATGACAGTCACTACAAATTAATATAGATGTGATG 518
Db 364 GCTGATGAACTGTGGTGTGTGGAAATGACAGTCACTACAAATTAATATAGATGTGATG 423
QY 519 GTTAAAGATGGCTCTTGGCGGAGTGCATTTTCTCTAATGAAAGCTTCTTGTCTACT 578
Db 424 GTTAAAGATGGCTCTTGGCGGAGTGCATTTTCTCTAATGAAAGCTTCTTGTCTACT 483
QY 579 GGGTCCCTCATGTGTGATTTAAACAGTGTGGAGTAAATGAGGCTCTGCATAGTGA 638
Db 484 GGGTCCCTCATGTGTGATTTAAACAGTGTGGAGTAAATGAGGCTCTGCATAGTGA 543
QY 639 AAGACATGATCTTGGAAATTAACCTGCTGCATTTTCTTCAAGCCAGTTTCTGATGA 698
Db 544 AAGACATGATCTTGGAAATTAACCTGCTGCATTTTCTTCAAGCCAGTTTCTGATGA 603
QY 699 GAAACAAGTCTTCAAGTTTTCGACTGGCATCATGTGCTCAGAGATTGCCAAGTCAAAAT 758
Db 604 GAAACAAGTCTTCAAGTTTTCGACTGGCATCATGTGCTCAGAGATTGCCAAGTCAAAAT 663
QY 759 TGGATGTTCTTCTTCCCATCTT----- 784
Db 664 TGGATGTTCTTCTTCCCATCTT----- 723
QY 785 ----- 784
Db 724 GGGCAGCTGCTGCTGTTGGCTTGTGCTTTTCCCATGATGGCGAGATGCTAGTCTCA 783
QY 785 ----- 784
Db 784 GGGTCAGTGGATAAGTCTGTATATATATGATACTAATAGTGAATATATCTTACACA 843
QY 785 ----- 784
Db 844 TTGACTCAGACACCAAGTATGTCACAACTTGTGCTTGGACCTTAATCCCTTTTACT 903
QY 785 ----- 784
Db 904 GCTACTGTTCAATGACAAAAACAGTGAACATCTGCAATTTGACCTGAAACACTTTGC 963
QY 785 --AGCAAGCGGCACAGAACTCAGCTGAGCAATTTACGAGATTGGTCAAGAGAGTCT 842
Db 964 CAAGCAAGCGGCACAGAACTCAGCTGAGCAATTTACGAGATTGGTCAAGAGAGAT 1023
QY 843 GTCCTCAACATGGCTTGTGACAAAGATTAAAGATCTTGTGGTATTTTCAAGATGAAT 902
Db 1024 GTTCTCAACATGGCTTGTGACAAAGATTAAAGATCTTGTGGTATTTTCAAGATGAAT 1083
QY 903 AACATTGATGAAAAAGAACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAA 962
Db 1084 AACATTGATGAAAAAGAACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAA 1143
QY 963 ATTGAATCTTGAAGACTGCTAGTAAAGTCTGAGGAAAAATTGAAGGCTCAGAGACCAAG 1202
Db 1144 ATTGAATCTTGAAGACTGCTAGTAAAGTCTGAGGAAAAATTGAAGGCTCAGAGACCAAG 1203
QY 1023 GTTAAATCCCTTCTTCAAGAAATCCGATGAATTTTATATGTCCAATTAAGTGAAGAACT 1082
Db 1204 GTTAAATCCCTTCTTCAAGAAATCCGATGAATTTTATATGTCCAATTAAGTGAAGAACT 1263
QY 1083 ATGAAAGATCCGTCATCGCATGAGATGCTATTCATATGAAAAAGAAAGATGAAAAAT 1142
Db 1264 ATGAAAGATCCGTCATCGCATGAGATGCTATTCATATGAAAAAGAAAGATGAAAAAT 1233
QY 1143 TGGATCAGCAAAAAGAAAGTACAGTCCATGACAAATCTTGTCTTCTTCAAGCGGTA 1202

Db 1324 TGGATCAGCAAAAAGAAAGTACAAAGTCCATGACAAATCTTGTCTTCTTCAAGCGGTA 1383
QY 1203 CTTACACCAAAATVGGCTCTGAAATGGCCATCAATAGTGGCTGGAGACACCAAAAG 1262
Db 1384 CTTACACCAAAATVGGCTCTGAAATGGCCATCAATAGTGGCTGGAGACACCAAAAG 1443
QY 1263 TAAA 1266
Db 1444 TAAA 1447
RESULT 12
AAD45076
ID AAD45076 standard; DNA; 1908 BP.
XX
XX AAD45076;
XX
XX 27-DEC-2002 (first entry)
XX
XX Human RET16.3 splice variant DNA.
XX
XX Human; RET16; intracellular signal; inflammation-related disease; asthma;
XX rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
XX transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
XX inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
XX inactive respiratory distress syndrome; cardiac; ulcerative colitis;
XX autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
XX cellular migration disorder; cell proliferation disorder; calcification;
XX hyperinulinemia; diabetes type 2; systemic lupus erythematosus; tumour;
XX cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
XX thalassemia; vasotropic; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT 136..1644
FT CDS /tag= a
FT /product= "Human RET16.3 splice variant protein"
XX
XX MO200266494-A2.
XX
XX 29-AUG-2002.
XX
XX 15-FEB-2002; 2002WC-US005162.
XX
XX 16-FEB-2001; 2001US-0269366P.
XX PR 29-MAY-2001; 2001US-0294181P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Todderud CG, Finger JN, Rillema J;
PI WPI; 2002-682760/73.
XX DR P-PSDB; AAE28168.
XX
XX New human, mouse or rat RET16 genes and proteins, involved in
PT intracellular signaling cascade, useful for in gene therapy, particularly
PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancer,
PT tumors or neoplasms.
XX
XX Claim 1; Page 168-169; 175pp; English.
XX
XX The invention relates to human, mouse or rat RET16 genes and proteins,
XX involved in intracellular signaling cascade. The RET16 protein or
XX polynucleotide is useful for treating an inflammation-related disease or
XX disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
XX asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
XX tissue transplants, chronic obstructive pulmonary disease, inflammatory
XX bowel disease, Crohn's disease, ulcerative colitis, inactive respiratory
XX distress syndrome, systemic lupus erythematosus, autoimmune disease,
XX cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
XX disease or disorder also includes disorders associated with aberrant
XX activation of the TNF-alpha pathway, disorders associated with aberrant

cellular migration, proliferation, metastasis, juvenile idiopathic arthritis, haemogenous metastases of tumour cells, hyperinsulinemia, diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer, tumour progression, Wegener's granulomatosis, stem cell transplantation complications, ischaemia-reperfusion injury, thalassemia, acute lung injury, graft rejection, ischaemic heart, coronary artery calcification or allergic inflammation. RET16 DNA is used in gene therapy. The present sequence is human RET16.3 splice variant DNA

XX Sequence 1908 BP; 550 A; 399 C; 405 G; 554 T; 0 U; 0 Other;

Query Match 69.0%; Score 877.8; DB 6; Length 1908;

Best Local Similarity 77.9%; Pred. No. 1.6e-257;

Matches 1253; Conservative 0; Mismatches 2; Indels 354; Gaps 2;

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QY 12 TCACCTGCGGGGCGACGTGACCCGACCGCCGCTGGGCACTTGAAGCGGATCCCGGCG 71
DB 37 TCACCTGCGGGGCGACGTGACCCGACCGCCGCTGGGCACTTGAAGCGGATCCCGGCG 96
QY 72 CCCCCGCTCGTGGAGGCTGTTTTCTTCAATAAAGAAACATGGTGAACATGATTCACACA 131
DB 97 CCCCCGCTCGTGGAGGCTGTTTTCTTCAATAAAGAAACATGGTGAACATGATTCACACA 156
QY 132 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
DB 157 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 216
QY 192 TGCTCTTGGACAAACAAATTCGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 251
DB 217 TGCTCTTGGACAAACAAATTCGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 276
QY 252 TCTCCATTGAAGTTCATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
DB 277 TCTCCATTGAAGTTCATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
QY 312 ATTTTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
DB 337 ATTTTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
QY 372 ATGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
DB 397 ATGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456
QY 432 GACTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
DB 457 GACTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516
QY 492 TCATACAAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
DB 517 TCATACAAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
QY 552 TCTCTTAATGAGAACTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
DB 577 TCTCTTAATGAGAACTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636
QY 612 GATTAATGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
DB 637 GATTAATGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
QY 672 TTTTCTTCAAGCAGTTTCTGATGAGAAACAGTCTTCAAGTTTTCAGTGGCATCA 731
DB 697 TTTTCTTCAAGCAGTTTCTGATGAGAAACAGTCTTCAAGTTTTCAGTGGCATCA 756
QY 732 TGTGTCAGAGTTCAGCAATCAAAATTTGATGATGATGATGATGATGATGATGATGAT 784
DB 757 TGTGTCAGAGTTCAGCAATCAAAATTTGATGATGATGATGATGATGATGATGATGAT 816
QY 785 ----- 784
DB 817 GAATTAATAATATAAAGTACAGTGAAGGCACTGTGCTCTGTTGCGCTTGCTTTT 876
QY 785 ----- 784
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DB 877 TCCCATGATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 936
QY 785 ----- 784
DB 937 ACTAATAGTGAATATATCTTCAACATGATGATGATGATGATGATGATGATGATGAT 996
QY 785 ----- 784
DB 997 GCTTTTGACCTAATACCTTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
QY 785 -----AGCAAGGCGCACAGAAACATGATGATGATGATGATGATGATGATGATGAT 815
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QY 967 -----AATCTTGA 977
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RESULT 13
AA160662/c
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XX
DT 22-OCT-2001 (first entry)
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DE Human polynucleotide SEQ ID NO 4651.
XX
KW Human; noctropic; immunosuppressant; cytosolic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukemia; ss.
XX
OS Homo sapiens.
XX
PN MO20015312-A1.
XX
PD 26-JUL-2001.
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XX 26-DEC-2000; 2000MO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
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PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehman T, Xu C, Xue AD, Yang Y, Zhang J, Zhao Q,
PI Zhou P, Goodrich R, Drmanac RT;
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XX MPI; 2001-44253/47.
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XX P-PSDB; AAM41506.
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PT Novel nucleic acid and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
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XX Claim 1; SEQ ID NO 4651; 10078pp; English.
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XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AAM38642-AAM42213) with neurotropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localized neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemoclastic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
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QY 1056 TTTATATGTCATAATCTAGAGAACTTAATGAAGATCCGCTCATGCTCATCAAGTGGCTAT 1115
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Db 1381 GTFAA 1385
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RESULT 15
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AC ADM19385;
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DT 20-MAY-2004 (first entry)
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DE Novel human channel/transporter gene #182.
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KW da; Gene: immunosuppressive; antiarthritic; antiheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KW optalmological; gene therapy; channel/transporter protein;
KW rheumatoid arthritis; neoplasm; cardiac arrest; cerebrovascular disorder;
KW cerebral ischemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.
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OS Homo sapiens.
XX
PN W0200154472-A2.
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GenCore version 5.1.6
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ALIGNMENTS

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ACCESSION	CR607851	GI:50486659				
VERSION	CR607851.1					
KEYWORDS	HTC; CNSLT_CDNA.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
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AUTHORS	L4,W.B., Gruber,C., Jesssee,J. and Polayes,D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished					
REMARK	Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue					
REFERENCE	2 (bases 1 to 1770)					
AUTHORS	Genoscope.					
TITLE	Direct Submission					
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqret@genoscope.cns.fr					
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a Noci-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.					
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 DB 609 TCTCTTAATGGAAGCTCTTGTCTACAGCTGCTCATGTGATGTTTAAACAGTGGAGAT 668
 QY 612 GATTAATAATGAGTGTCTGATAGTGAATAAGCAATGATCTTGAATTAACCTGTGCGAT 671
 DB 669 GATTAATAATGAGTGTCTGATAGTGAATAAGCAATGATCTTGAATTAACCTGTGCGAT 728
 QY 672 TTTTCTTCAACAGCAGTCTTCTGATGGAACAGAGTCTTCAATTTTTCAGCTGCGATCA 731
 DB 729 TTTTCTTCAACAGCAGTCTTCTGATGGAACAGAGTCTTCAATTTTTCAGCTGCGATCA 788
 QY 732 TGTGCTCAGAGTGGCCAGTCAAAATTTGATGTTTCTTTTACCCTATCTT----- 784
 DB 789 TGTGCTCAGAGTGGCCAGTCAAAATTTGATGTTTCTTTTACCCTATCTT----- 848
 QY 785 ----- 784
 DB 849 GAATTAATAATATAAGTACACTGATGAGGCACTGTGCTCTGTTCTGAGCTTGTGCTTTT 908
 QY 785 ----- 784
 DB 909 TCCCATGATGAGGAGATGATGCTCAGAGTCAAGGTCAAGTGAATGCTGTCAATATATGAT 968
 QY 785 ----- 784
 DB 969 ACTAATACTGAGAAATATCTTCAACATGTGACTCAGACACAGATATGTCACAACTTGT 1028
 QY 785 ----- 784
 DB 1029 GCTTTTGCACCTAATACCTTTTACTTGTACTGTTCAATGGAACAAACAGTGAACATC 1088
 QY 785 -----AGCAAGGCGCACAAACATCAGCTGGAACAA 815
 DB 1089 TGGCAATTTGACCTGGAACAACTTTGCAAGGAGGCGCACAGAAACATCAGCTGGAACAA 1148
 QY 816 TTTTACCGAAGATTGTCAGAGAGAGTGTCTCAACATGAGCTTTGTGCAAGAGATTAAAA 875
 DB 1149 TTTTACCGAAGATTGTCAGAGAGAGTGTCTCAACATGAGCTTTGTGCAAGAGATTAAAA 1208

QY 876 GATCTTGTGTAATTTTCAAGATGATAACATTGATGAGAAAAGAACTGTGATCTTACA 935
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 DB 1449 TCAATGAAAAGAAAGCAATGGAATTTGATGACGAAAAAGAAAGCTACAGTCCCATG 1508
 QY 1176 ACAATCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1235
 DB 1509 ACAATCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1568
 QY 1236 AATGATGCTGTGAGACACACCAAAAGTAAA 1266
 DB 1569 AATGATGCTGTGAGACACACCAAAAGTAAA 1599
 RESULT 2
 CR619104 1600 bp mRNA linear HTC 21-JUL-2004
 LOCUS Full-length cDNA clone CS0D1075YB08 of Placentia Coc 25-normalized
 DEFINITION of Homo sapiens (human).
 CR619104
 ACCESSION CR619104.1 GI:50499911
 VERSION HTC; CDSUT_CDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1600)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polajec, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1600)
 REFERENCE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1075YB08"
 /tissue_type="Placentia Coc 25-normalized"
 /plasmid="pCMVSPORT_6"
 ORIGIN
 Query Match 61.5%; Score 782; DB 3; Length 1600;
 Best Local Similarity 77.3%; Pred. No. 1,6e-212;
 Matches 1075; Conservative 0; Mismatches 180; Indels 135; Gaps 5;

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QY 12 TCACCTGCGGCGACGCGACCCGACCGCGGACCTTGAAGGCGGATCCCGCG 71
DB 13 TCACCTGCGGCGACGCGACCCGACCGCGGACCTTGAAGGCGGATCCCGCG 72.
QY 72 CCCCCTCTCTGAGGCTGTTTTCTTCAATAAAGAACTGGTGAATGATTCACACA 131
DB 73 CCCCCTCTCTGAGGCTGTTTTCTTCAATAAAGAACTGGTGAATGATTCACACA 132
QY 132 TTAGCTGATCATGTGACGATGTCACACTGCTGCTCTCTCTCTCTCTCTCTCT 131
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QY 192 TGCTCTTGACAAACAATTCGCTGTACTGCTGTACTGCTGTACTGCTGTACTG 251
DB 193 TGCTCTTGACAAACAATTCGCTGTACTGCTGTACTGCTGTACTGCTGTACTG 252
QY 252 TCTCCATTGAAAGTTTCAATCTTACCTTACCTTACCTTACCTTACCTTAC 311
DB 253 TCTCCATTGAAAGTTTCAATCTTACCTTACCTTACCTTACCTTACCTTAC 312
QY 312 ATTTTGGCATCTGTTCAAGATGTCACACTGCTGTACTGCTGTACTGCTGT 371
DB 313 ATTTTGGCATCTGTTCAAGATGTCACACTGCTGTACTGCTGTACTGCTGT 372
QY 372 ATGCTGGCATGATGGAACAGCCCTAGTGGAGCGGCTGTGAGGCTTTCAGTT 431
DB 373 ATGCTGGCATGATGGAACAGCCCTAGTGGAGCGGCTGTGAGGCTTTCAGTT 432
QY 432 GACTCCACGTTTGGCATGAGGCGGACGCTGATGGAACGTTGTTTGGAAATG 491
DB 433 GACTCCACGTTTGGCATGAGGCGGACGCTGATGGAACGTTGTTTGGAAATG 492
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QY 552 TCCTCTTAATGGAAGCTCTTGTCTACAGTGGCTCTCTCATGCTGTGTTTAA 611
DB 553 TCCTCTTAATGGAAGCTCTTGTCTACAGTGGCTCTCTCATGCTGTGTTTAA 612
QY 612 GATTAATGAGGTCTCTCATAGTGAAGAAAGCAATGATCTTGAATTAACCT 671
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QY 672 TTTTCTTCAACAGCAGTTTCTGATGGAAGAAAGCTCTTCAATTTTCACT 731
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QY 732 TGTGTCAGGATGCGCAAGTCAAAATTTGATGTTCTTTTACCCTATCTTGA 791
DB 733 TGTGTCAGGATGCGCAAGTCAAAATTTGATGTTCTTTTACCCTATCTTGA 792
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DB 793 GAATTAATAATATAAGATACAGTGAAGGCACTGCTCTGTTGCGGCTGTGCT 852
QY 819 ACCGAAGATTGGTCAAGGAGGCT----- 842
DB 853 TCCCATGATGGGAGATGCTAGTCTCAGGCTCAGTGATAGTCTGCTCATATAT 912
QY 843 -----GCTCAACATG 854
DB 913 ACTAATATCTAGATATATCTTACACACTTGAAGTCAACAGTATGTCACAACT 972
QY 855 CTTTTGTGACAGAA-----TTTAAAGATCTTGTGATTTTCAAGATGAATTA 908
DB 973 GCTTTTGCACCTAATACCTTTTCTGCTAAGTGTGATGACAAACAGTGAAC 1032
QY 909 GATGGAAGAAAGCTGTTGATCTTCAAAAGAAAGTCTGCTGATGATTTGAA 968
DB 1033 TGGCAATTTTGAATCTGGAAGAACTTTGCGCAAGGCGCAGAAACATCACT 1092
QY 969 TCT--CTAGAGCTGCTGATGTAAGTGTGAGGAATTTGAAGAGCTCAGAAC 1026

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DB 1093 TTTACGGAAGATTGGTCAAGAGAGATGCTCAACATGCTTTGTGACAAAGATTTAA 1152
QY 1027 AATCCCTTTCTTCAAGAAATTCCTGATGATTTATATGTCATTAATCTAGAACTTA 1086
DB 1153 GATCTTTGTTGGTATTTTCAAGATGAATTAACATGATGGAAGAAAGCTGTAATCTT 1212
QY 1087 AA-----GATCCGGCATGCGATGATGAGGCTATTCATATGAAAGAAAGCAATG 1136
DB 1213 AAAGAAAGTCTGCTGATGATTTGAAATTTGATGAGGCTATTCATATGAAAGAAAGCA 1272
QY 1137 GAAATTTGATGACAAAGAAAGAAAGCTACAAAGTCCCATGACAAATCTTCTCTCTCA 1196
DB 1273 GAAATTTGATGACAAAGAAAGAAAGCTACAAAGTCCCATGACAAATCTTCTCTCTCA 1332
QY 1197 GCGGTAATTAACCAAAATAGGACTTGAAGAAATGCGCATATATGATGCTGAGACAC 1256
DB 1333 GCGGTAATTAACCAAAATAGGACTTGAAGAAATGCGCATATATGATGCTGAGACAC 1392
QY 1257 CAAGATTA 1266
DB 1393 CAAGATTA 1402

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RESULT 3
LOCUS AL533510 941 bp mRNA linear EST 24-MAR-2004
DEFINITION AL533510 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
ACCESSION CS0DN004YJ15.5-PRIME, mRNA sequence.
VERSION AL533510
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 941)
JOURNAL Pull-length cDNA libraries and normalization
Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:31260591.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1653.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0DN004YJ15&c=1653.r.
Location/Qualifiers
1. 941

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FEATURES
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1. 941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN004YJ15"
/issue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN

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Query Match 60.3%; Score 767.4; DB 1; Length 941;
Best Local Similarity 98.7%; Pred. No. 2e-208;
Matches 765; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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QY 12 TCACCTGCGGCGACGTGACCCGACCGCCGCGGACCTTGAGGCGGATCCCGCG 71
Db 68 TCCCTCGCGGCGACGTGACCCGACCGCCGCGGACCTTGAGGCGGATCCCGCG 127
QY 72 CCCCCCTCTGCAAGCTGTTTTTCTTCAATTAAGAACTGGTGAACGTATTCACACA 131
Db 128 CCCCCCTCTGCGGCGCTGTTTTTCTTCAATTAAGAACTGGTGAACGTATTCACACA 187
QY 132 TTAGCTGATCATGATGACGATGTCACACTGCTGTCCTCTTCCCTTCCCTGGCTACT 191
Db 188 TTAGCTGATCATGATGACGATGTCACACTGCTGTCCTCTTCCCTTCCCTGGCTACT 247
QY 192 TGTCTCTTGACAAACAATTCGCTGTACTGCTTAAGTACTGAATCCACAT 251
Db 248 TGTCTCTTGACAAACAATTCGCTGTACTGCTTAAGTACTGAATCCACAT 307
QY 252 TCTCCATTGAAGTTTATACCTTAAGCTGTCACACTGCTGCTTCCCTTCCCTGACAT 311
Db 308 TCTCCATTGAAGTTTATACCTTAAGCTGTCACACTGCTGCTTCCCTTCCCTGACAT 367
QY 312 ATTTGGCATTCGTTTCAACAGATGAGTACCACTGCTCTATGAAATGAAATGACAG 371
Db 368 ATTTGGCATTCGTTTCAACAGATGAGTACCACTGCTCTATGAAATGAAATGACAG 427
QY 372 ATGCTGCGAGTGTGAAGACGCTAGTGGCAGCCCTGTGAGGGTTTGCAGTTTCCCA 431
Db 428 ATGCTGCGAGTGTGAAGACGCTAGTGGCAGCCCTGTGAGGGTTTGCAGTTTCCCA 487
QY 432 GACTCCACGTTTGGCATTCAGGGGCGAGCTGTAGTGAATCTGTTTGTGATGACAG 491
Db 488 GACTCCACGTTTGGCATTCAGGGGCGAGCTGTAGTGAATCTGTTTGTGATGACAG 547
QY 492 TCATACAAATTATATAGATGTGTAGTGTAAAGATGCTCTTGGGCGCATGTCATT 551
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QY 552 TCTCTTAATGGAAGCTTCTTTGTCACTGCTCTCATGTGGAATTAACAGTGGAGT 611
Db 608 TCTCTTAATGGAAGCTTCTTTGTCACTGCTCTCATGTGGAATTAACAGTGGAGT 667
QY 612 GATAAAATGAGGTGTGCTGATGTAAGAAAGCAATGATTTGGATTAACCTGCGAT 671
Db 668 GATAAAATGAGGTGTGCTGATGTAAGAAAGCAATGATTTGGATTAACCTGCGAT 727
QY 672 TTTTCTTCAAGCAGCTTTCTGATGAGAAACAAGCTTCACTTTTTCAGTGGCATCA 731
Db 728 TTTTCTTCAAGCAGCTTTCTGATGAGAAACAAGCTTCACTTTTTCAGTGGCATCA 787
QY 732 TGTGTGACAGATTTGCCAAGTCAAAATTTGGATGTTTCTTTAACCATATCTTAG 786
Db 788 TGTGTGACAGATTTGCCAAGTCAAAATTTGGATGTTTCTTTAACCATATCTTAG 842

RESULT 4
AL553333 889 bp mRNA linear EST 30-MAR-2004
LOCUS AL553333 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1075B08 5-PRIME, mRNA sequence.
ACCESSION AL553333
VERSION AL553333.3 GI:45858102
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 889)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31275147.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
```

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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1653.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1075D040&pic=1653.r.
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Query Match 59.5%; Score 756.6; DB 1; Length 889;
Best Local Similarity 99.0%; Pred. No. 2.5e-205;
Matches 767; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
QY 12 TCACCTGCGGCGACGTGACCCGACCGCCGCGGACCTTGAGGCGGATCCCGCG 71
Db 13 TCASCTGSGGCGACGTGACCCGACCGCCGCGGACCTTGAGGCGGATCCCGCG 72
QY 72 CCCCCCTCTGCAAGCTGTTTTTCTTCAATTAAGAACTGGTGAACGTATTCACACA 131
Db 73 CCCCCCTCTGCAAGCTGTTTTTCTTCAATTAAGAACTGGTGAACGTATTCACACA 132
QY 132 TTAGCTGATCATGATGACGATGTCACACTGCTGTCCTCTTCCCTTCCCTGGCTACT 191
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QY 192 TGTCTCTTGACAAACAATTCGCTGTACTGCTGTTAAGTAACTGAACGTCCACAT 251
Db 193 TGTCTCTTGACAAACAATTCGCTGTACTGCTGTTAAGTAACTGAACGTCCACAT 252
QY 252 TCTCATTAAGTTTATACCTATGCTGTCACTGCTGCTGTTTCCCTTCAGACAT 311
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Db 373 ATGCTGCGAGTGTGAAGACGCTAGTGGCAGCCCTGTGAGGGTTTGCAGTTTTCGCC 432
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Db 493 GTCATCAAAATTATATAGATGTGTGTTTAAAGATGCTCTTGGCGGATGTCATT 552
QY 551 TTCTCTTAATGGAAGTTTCTTGTCACTGCTGCTCTCAATGTTGATTAACGTGGGGA 610
Db 553 TTCTCTTAATGGAAGTTTCTTGTCACTGCTGCTCTCAATGTTGATTAACGTGGGGA 612
QY 611 TGATAAAATGAGGTGCTCATAGTGAATAAGACATGATCTTGAATTAACGTGCGGA 670
Db 613 TGATAAAATGAGGTGCTCATAGTGAATAAGACATGATCTTGAATTAACGTGCGGA 672
QY 671 TTTTCTTCAAGCCAGTTTCTGATGGAACAAGTCTTCACTTTTTCAGTGGCATC 730
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Qy	731	ATGTGTCAGAGATTCCCAATGCAATTAATTGGATTGTTCTTTTACCATATCTTA	785
Db	733	ATGTGTCAGAGATTCCCAAGTCAAAATTTGGATTGTTCTTTTACCATATCTTA	787
RESULT 5			
LOCUS	BM543484		
DEFINITION	BM543484	1010 bp	mRNA
ACCESSION	AGENCOURT 6492519	NIH_MGC_124	Homo sapiens cDNA clone IMAGE:57265722
KEYWORDS	5', mRNA sequence.		
SOURCE	BM543484		
ORGANISM	BM543484.1	GI:18773915	EST.
REFERENCE	Homo sapiens (human)		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 1010)		
COMMENT	NIH-MGC http://mgs.nci.nih.gov/.		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Invitrogen		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.gov		
	Plate: LHAM12719	row: e	column: 05
	High quality sequence start: 6		
	High quality sequence stop: 669.		
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	/issue_type="hippocampus"		
	/lab_host="DH10B"		
	/clone_id="NIH_MGC_124"		
	/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV		
	(destroyed); Site 2: NotI; RNA source male hippocampus,		
	age 27. Library is oligo-dT primed and directionally		
	cloned (EcoRV site is destroyed upon cloning). Average		
	insert size 1.4 kb, insert size range 0.9-4 kb. Library is		
	normalized and enriched for full-length clones and was		
	constructed by C. Gruber (Invitrogen). Research Genetics		
	tracking code 012."		
ORIGIN			
Query Match	56.3%	Score 716.6	DB 4; Length 1010;
Best Local Similarity	97.6%	Pred. No. 7.9e-194;	
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Db	87	TCACCTGGGGGCGACGTACCCCGCACCCCGCGTGGGACCTTGAAGGCGATCCCGCGG	146
Qy	72	CCCCGGCTCCGACAGGCTGTTTTCTTCAAAATAAAGACATGGGAACATGATTCACACA	131
Db	147	CCCCGGCTCCGACAGGCTGTTTTCTTCAAAATAAAGACATGGGAACATGATTCACACA	206
Qy	132	TTAGTGATCATGTGACGATGTCAACTGCTGTGCTTCTCTTTTCCCTCTTGCTACT	191
Db	207	TTAGTGATCATGTGACGATGTCAACTGCTGTGCTTCTCTTTTCCCTCTTGCTACT	266
Qy	192	TGCTCTTGGACAAACAATTGCGCTGTACTCTGTAAGTGAATTAAGTAAGTGGACAT	251
Db	267	TGCTCTTGGACAAACAATTGCGCTGTACTCTGTAAGTGAATTAAGTAAGTGGACAT	326

Oy		252	TCTCCATGTAAGTTTCACTACTATATGCCTGCACGTGGCTGTTTCGCCCTTGAGCAT	311
Db		327	TCTCATTGAAGTTTCACTACTATATGCCTGCACGTGGCTGTTTCGCCCTTGAGCAT	386
Oy		312	ATTTTGGCAGTCGTTTCMACAGATGGTAGCACGTGCTCTATGAGATACTGAAAAATGACAG	371
Db		387	ATTTTGGCAGTCGTTTCMACAGATGGTAGCACGTGCTCTATGAGAAATACTGAAAAATGACAG	446
Oy		372	ATGTGGCAGTATGGAACAGCCTAAGTGGAGACCCTGTAGAGGTTTGCCAGTTTTCCCACA	431
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Oy		432	GACTCCACGCGTTTGGCATCAGGGGACGCTGATGGAACCTGNGGTTTGTGGAATGACAG	491
Db		507	GACTCCACGCGTTTGGCATCAGGGGACGCTGATGGAACCTGNGGTTTGTGGAATGACAG	566
Oy		492	TCATACCAATTAATATAGATGTGTAGTGTAAAGATGGCTTCCTTGGCGGACATGTGATTT	551
Db		567	TCATACCAATTAATATAGATGTGTAGTGTAAAGATGGCTTCCTTGGCGGACATGTGATTT	626
Oy		552	TCCTCTAATGGAAGCTTCTTTGTACATGCTGCTCTCATATGTGTATTTAACATGTGGAT	611
Db		627	TCCTCTAATGGAAGCTTCTTTGTACATGCTGCTCTCATATGTGTATTTAACATGTGTGGAT	686
Oy		612	GATPAAAATGAGGTGTGTGCAATAGTAAAAAGCA-CATGATCTTGGAAATPACCTGTGGCA	670
Db		687	GATPAAAATGAGGTGTGTGCAATAGTAAAAAGCAATGATCTTGGAAATPACCTGTGGCA	746
Oy		671	TTTTTCTTCAAGCCATTTTCTGATGAGAACA--GCTCTTCAAGTTTTTTCAGTGGCA	728
Db		747	TTTTTCTTCAAGCCGTTTCTGATGAGAACAAGTCTTCCAGTTTTTTTTCGAATGGCA	806
Oy		729	TCATGTGTCAGAGATTGCCAAGTCAAAA--TTTGGATTGTTTCTTTAACCATATCTTA	785
Db		807	TCATGTGTCAGAGATTGCCAAGTCAAAAATTTGGAATTTGTTCTTTAACCATATCTTTA	865
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LOCUS			60324982BF1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301559 5'	
DEFINITION			mRNA sequence.	
ACCESSION			B1603184	
VERSION			B1603184.1 GI:15496123	
KEYWORDS			EST.	
SOURCE			Homo sapiens (human)	
ORGANISM			Homo sapiens	
REFERENCE			Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE			NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL			National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT			Unpublished (1999)	
			Contact: Robert Strausberg, Ph.D.	
			Email: rgs@fda.fda.gov	
			Tissue Procurement: Miklos Palokovits, M.D., Ph.D.	
			cDNA Library Preparation: Michael J. Brownstein (NHRI), Shiroki	
			Toshuyuki and Piero Carninci (RIKEN)	
			cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)	
			DNA Sequencing by: Incyte Genomics, Inc.	
			Clone distribution: MGC clone distribution information can be	
			found through the I.M.A.G.E. Consortium/LNLN at:	
			http://image.llnl.gov	
			Plate: LHAM1763 row: h column: 08	
			High quality sequence stop: 756.	
			Location/Qualifiers	
			1..858	
FEATURES			/organism="Homo sapiens"	
source			/mol_type="mRNA"	
			/db_xref="taxon:9606"	
			/clone="IMAGE:5301559"	
			/issue_type="hypothalamus"	

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/lab host="DH08"
/clone.lib="NIH_MGC_96"
/note="Organ: brain; Vector: Bluescript (modified
           plasmid KS+); Site_1: BamHI; Site_2: SalI-XhoI
           (gtagag); Oligo-dt primed using primer
           5'-TTTTTTTTTTTTTTTT-3', size-selected for average
           insert size 2.3 kb and normalized to R07 5. This is a
           primary library enriched for full-length clones and
           constructed using the Cap-trapper method (Carninci, in
           preparation). Library constructed by M. Brownstein
           (NIH/NHGRI, National Institutes of Health). Note: this is
           a NIH_MGC library."

```

```

/clone_1b="NIH MGC 96"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gcg96); Oligo-dT primed using primer:
5'-TTTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
NIH MGC Library."

```

5'-TTTTTTTTTTTTTTTTTTN-3', size-selected for average insert size 2.3 kb and normalized to R05. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carnicci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

ORIGIN

Query Match	Similarity	52.2%	Score	664.2	DB 4	Length	858	
Best Local	Similarity	93.9%	Pred.	No.	8.2e-179			
Matches	Conservative	0	Mismatches	38	Indels	11	Gaps	6
QY	12	TCACCTGCGCGGACGTGACCCCGACCGCCCGTGGGCACTTTGAAGCGGATCCCGCGC	71					
Db	52	TCACCTGCGCGGACGTGACCCCGACCGCCCGTGGGCACTTTGAAGCGGATCCCGCGC	111					
QY	72	CCCCCGCTCTGCAAGCGCTTTTCTTGAATTAAGAACATGGTGAACCTGATTCACACA	131					
Db	112	CCCCCGCTCTGCAAGCGCTTTTCTTGAATTAAGAACATGGTGAACCTGATTCACACA	171					
QY	132	TTAGCTGATCATGTGTGACGATGTCAACTGTGTGCTTCTCTCTTTCCCTGTGGCTACT	191					
Db	172	TTAGCTGATCATGTGTGACGATGTCAACTGTGTGCTTCTCTCTTTCCCTGTGGCTACT	231					
QY	192	TGCTCTCTGGAACAAACAAATTCGCTGTACTCTGTTAAGTGAATTAAGTGAACCTGACAT	251					
Db	232	TGCTCTCTGGAACAAACAAATTCGCTGTACTCTGTTAAGTGAATTAAGTGAACCTGACAT	291					
QY	252	TCTCATTTGAAGTTTCACTATACCTATGCTGTCTGCACTGCTGTTTCTCCCTTCAGACAT	311					
Db	292	TCTCATTTGAAGTTTCACTATACCTATGCTGTCTGCACTGCTGTTTCTCCCTTCAGACAT	351					
QY	312	ATTTTGGCATGCTGTTCAACAGATGTAACACTGTCTATGGAATTAAGTGAACCTGACAG	371					
Db	352	ATTTTGGCATGCTGTTCAACAGATGTAACACTGTCTATGGAATTAAGTGAACCTGACAG	411					
QY	372	ATGCTGGAGAGATGGAACACGCTTAAGTGGACGCGCTGTGAAGGTTTGGCACTTTTCCCA	431					
Db	412	ATGCTGGAGAGATGGAACACGCTTAAGTGGACGCGCTGTGAAGGTTTGGCACTTTTCCCA	471					
QY	432	GACTTCCACGCTTTGGCATTCAGGGGCAAGCTGATGAACTGTGTGTTTGGGAATGACAG	491					
Db	472	GACTTCCACGCTTTGGCATTCAGGGGCAAGCTGATGAACTGTGTGTTTGGGAATGACAG	531					
QY	492	TGATTAACAAATTATATAGATGTGTGTATGTTAAAGATGGCTCCTTGGCGGATGTGCATTT	551					
Db	532	TGATTAACAAATTATATAGATGTGTGTATGTTAAAGATGGCTCCTTGGCGGATGTGCATTT	591					
QY	552	TCTCCTTAATGGAAGGCTCTTTGTGCACTGGCTCTCATGTGGGATTTTAAACAGTGGGAT	611					
Db	592	TCTCCTTAATGGAAGGCTCTTTGTGCACTGGCTCTCATGTGGGATTTTAAACAGTGGGAT	651					
QY	612	GATTAATAATGA-GGTGCTGTCAATAGTGAATAAAGACATGATCTTGGAAATTC--GTGCT	666					
Db	652	GATTAATAATGAAGGCTGTGCAATAGTGAATAAAGACATGATCTTGGAAATTCCTGCTGCC	711					
QY	667	GCGATTTTCTTTCACAGCCAGCTTTGTGA-TGGAGAACAAAGGCTTCA--GTTTTTGGAC	723					
Db	712	GATTTTCTTTCACAGAGCAAGCTCTGTGATTGGAGAACAAAGGCTTTCAGAGTTTTTTCGAC	771					
QY	724	TGGCATC--ATGTGTGAGGATTTGGCAAGT-CAAAATTTGGAATGTTTCTTTTACCATTA	780					
Db	772	TGGCATCATGTGTGCTGCAGGATTTGGCAAGTCCAAATTTGGAGTGGTCTTTTACCGATA	831					
QY	781	TCTTAAGCAAGGCGCACAAACATCAGC	807					
Db	832	TCTTAAGCAAGGCGCACAAACATC	858					

FEATURES	SOURCE
LOCUS	B1821143
DEFINITION	B1821143 792 bp mRNA linear EST 04-OCT-2001
ACCESSION	60305030F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176086 5',
VERSION	B1821143
KEYWORDS	B1821143.1 GI:15932693
WORD	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL	1 (bases 1 to 792)
COMMENT	NIH-MGC http://imgc.ncl.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cgabs-r@mail.nih.gov
	Tissue Procurement: Life Technologies, Inc.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LNL at:
	http://image.lnl.gov
	Plate: L14M1438 row: 1 column: 07
	High quality sequence stop: 751.
	Location/Qualifiers
	1..792

FEATURES

Source

ORIGIN

Query Match	49.3%	Score 627, 4; DB: 168	Length 792;
Best Local Similarity	96.4%	Pred. No. 2, 96-168	
Matches 749;	Conservative 0;	Mismatches 16;	Indels 12; Gaps 10;
QY	12	TCACCTGCGCGGACGATGACCCGACCGCCGCGGACCTTGAGGCGGATCCGCGCG	71
DQ	20	TCACCTGCGCGGACGATGACCCGCGGACCG - CGATGCGACCTTGAGGCGGATCCGCGCG	78
QY	72	CCCCCGCTCCTGCGAGCGCTGTTTTCTTCAATATAGAAACATGGTGAACATGATTCACACA	131
DQ	79	CCCCCGCTCCTGCGAGCGCTGTTTTCTTCAATATAGAAACATGGTGAACATGATTCACACA	138
QY	132	TTAGCTGATCATGGTGACGATGTCACCTGCGTGCCTTCTCCTTTTCCCTTGGATCACT	191
DQ	139	TTAGCTGATCATGGTGACGATGTCACCTGCGTGCCTTCTCCTTTTCCCTTGGATCACT	195
QY	192	TGCTCTTGGACAACAACAATTCGGCTGTACTCGTTACGTGACTTTTACTGAACTTCCACAT	251
DQ	196	CTGCTCTTGGACAACAACAATTCGGCTGTACTCGTTACGTGACTTTTACTGAACTTCCACAT	255
QY	252	TTCTCATTGAAGTTTCTTACTCTATAGCTGTCGACGCGCGCTGTTTCTGCCCTTGAGGACAT	311
DQ	256	TTCTCATTGAAGTTTCTTACTCTATAGCTGTCGACGCGCGCTGTTTCTGCCCTTGAGGACAT	315

Query Match	Best Local Similarity	Matches	Score	DB	Length
87	41.5%	527	8	728	
78	88.2%	574	119	77	0
147					
138					
207					
198					
267					

	RESULT 9	
	A1189142	
	LOCUS	
	A1189142	
	505 bp	mrna
		linear
		EST 13-OCT-1998
Oy	327	TCACAGATGGTACCTGTCCTCATGGAATACGAAATGGACAGATGCTGGCAGTATG 386
Db	318	TCACAGATGGTACCTGTCCTCATGGAATACGAAACGGCGAGATTCTGGCAGTATG 377
Oy	387	GAACAGCCCTAGTGGCAGCCCTGTGAGGGTTTGGCAGTTTCCCAAGCTCCAGCTGTTTG 446
Db	378	GAACAGCCCTAGTGGTACCCCTGTGAGAGTGGCCGATTCTCCCAAGCTCCAGCTGTTTG 437
Oy	447	GCATCAGGGGACAGCTGATGGAACCTAGTGGTCTTGTGGAATGCACAGTATACAATATATAT 506
Db	438	GTCGACAGGGGATCTGATGGAACTGTTGTTTGTGGAATGCACAGTATACAATATATAT 497
Oy	507	AGATGTGTAGTGTTTAAAGATGGTCTCTTGGCGGCATGTGCATTTTCTCTTAATGGAAGC 566
Db	498	AGAGTGTCTGTGTGTTAAGATGGTCTCTTGTGGCGCCTGTGGTCTTCTCTCCGGAAC 557
Oy	567	TTCTTTTTCATCGGCTCTCATGTGGATTTAAACAGTGTGGAGTGAATAAATGAGGTGT 626
Db	558	CTCTTTTTCATCGGCTCTCATGTGGATTTAAACAGTGTGGAGTGAATAAATGAGGTGT 617
Oy	627	CTGATATGTGAAAAAGCAGATGATCTTGGATTACCTGCTGCCAATTTTCTTCCACAGCA 686
Db	618	CTGACAGTGTAAAAAGCAGATGATCTTGGATTACCTGCTGTGACTTTTCTTCCACACCA 677
Oy	687	GTTTCTGATGAGAACAGGCTCTCAGTTTCTTTTTCGATGGCAGCATATGTGT 737
Db	678	GTTCTGTGTGAGAACAGAGGCTCTCAGTTTCTTTTCAGTTGGCATATGTGT 728

DEFINITION	gqdaa4.x1 Soares placenta BC095968.2BHB88CCOM Homo sapiens cDNA clone IMAGE:1722702 3' similar to SM:TDD3 DROME P49846 TRANSCRIPTION INITIATION FACTOR TFIIID 85 KD SUBUNIT 1, mRNA sequence.
ACCESSION	A1189142
VERSION	A1189142.1 GI:3740351
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE	Nci-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT	Tumor Gene Index Unpublished (1997) Contact: Robert Strusberg, Ph.D. Email: cgephs-remail.nih.gov This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Glibco High quality sequence stop: 421. Location/Qualifiers 1..505
FEATURES	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1728702" /dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares_placenta_8to9weeks_2NHPEPOM" /note="Organ: Placenta; Vector: pTRIS3 (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGGCCGCAGATTGTGTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia) , digested with Not I and cloned into the Not I and Eco RI sites of a modified pTRIS3 vector (Pharmacia) . Library constructed by Bento Soares and M.Fatima Bonaudo."
ORIGIN	
Query Match	38.8%; Score 493; DB 1; Length 505;
Best Local Similarity	39.8%; Pred. No. 9.1e-130; Indels 1; Gaps 1,
Matches 504; Conservative 0; Mismatches 0;	
QY	96 CTTCAAAATAAAGAACAATGTAAGTCACACATTAGTCATGTCAGCATGTC 155
Db	1 CTTCAAAATAAAGAACAATGTAAGTCACACATTAGTCATGTCAGCATGTC 60
QY	156 AACTGCTGTGCTCTCCCTTTCCCTCTGCTACTGCTCCTTGGACAAAACAATTGCG 215
Db	61 AACTGCTGTGCTCTCCCTTTCCCTCTGCTACTGCTCCTTGGACAAAACAATTGCG 120
QY	216 CTGTAAGTGTAGTAGTACTTACTGAATCGCACATTCATCTGAATGAATTCATCTAT 275
Db	121 CTGTAAGTGTAGTAGTACTTACTGAATCGCACATTCATCTGAATGAATTCATCTAT 180
QY	276 GCTGTCCACCTGCTGTTTCTCCCTTCAGACATATTTTGGATCGTGTTCACACAT 335
Db	181 GCTGTCCACCTGCTGTTTCTCCCTTCAGACATATTTTGGATCGTGTTCACACAT 240
QY	336 GGTAACAATGTCATATGTAATACTGAATAATGACAGATGTCGCGAGTATGGAACAGCT 395
Db	241 GGTAACAATGTCATATGTAATACTGAATAATGACAGATGTCGCGAGTATGGAACAGCT 300
QY	396 AGTGGACACCCTGTGAGGCTTTCGACGATTTTCCCAGACTCCACGCTGTTGGCATCAGGG 455
Db	301 AGTGGACACCCTGTGAGGCTTTCGACGATTTTCCCAGACTCCACGCTGTTGGCATCAGGG 360
QY	456 GCAGGTATGGAACCTGGG- TTTTGTGGAATGACAGCATACAAATTAATATGATGTGG 514
Db	361 GCAGGTATGGAACCTGGGTTTGTGGAATGACAGCATACAAATTAATATGATGTGG 420
QY	515 TAGTGTAAAGATGGCTCTTGGCGGACATGTGCATTTTCTCTAATGGAAGCTTCTTGT 574
Db	421 TAGTGTAAAGATGGCTCTTGGCGGACATGTGCATTTTCTCTAATGGAAGCTTCTTGT 480
QY	575 CACTGGCTCTCATATGTGGTATTTA 599
*	

Db	481	CACGTGGCTCCATGTGTGATTTTA	505
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BX282729	NIH MGC 116 Homo sapiens	cdNA clone	IMAGE5187309 ;
DEFINITION	IMAGE:5187309, mRNA sequence.		
ACCESSION	BX282729		
VERSION	BX282729.1	GI:28615370	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 499) Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.		
TITLE	Human Unigeneset - RZPD3		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGE59802211467. RZPDLIB; I.M.A.G.E. cDNA clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi- bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M3u, Primer sequence: CGTTGTAAACGACGCCACT.		
FEATURES	Location/Qualifiers		
Source	1..499 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE59802211467 ; IMAGE:5187309" /lab_host="DH10B" /clone_lib="NIH_MGC_116" /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-Sportc; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of ; stomach, 62 yo male and 70 yo female. Library is: oligo-dT primed and directionally cloned (EcoRV site in destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	38.2%; Score 486.2; DB 5; Length 499;		
Best Local Similarity	99.4%; Pred. No. 8.1e-128;		
Matches	488; Conservative 0; Mismatches 3; Indels 0; Gaps 0		
Oy	296	CTCCCTTCAGAGATATTTTGGCATCGTGTTCACACAGATGTACCACTGTCCTATGGA	355
Db	1	CGCTCTCGACGACATATTTTGGCATCTGTTCACACAGATGTACCACTGTCCTATGGA	60
Oy	356	TACTGAAATGACAGATGCTGGCAGTGATGGAACAGCCTTAGTGCAAGCCTTGAGAGGT	415
Db	61	TACTGAAATGACAGATGCTGGCAGTGATGGAACAGCCTTAGTGCAAGCCTTGAGAGGT	120
Oy	416	TTGCGAGTTTCCCGACGATCCAGTGTGTTGGCATCAGGGCAGGTGATGGAACGTGTGT	475
Db	121	TTGCGAGTTTCCCGACGATCCAGTGTGTTGGCATCAGGGCAGGTGATGGAACGTGTGT	180

QY 476 TTGTGGAATGCACAGTCATCAAAATTATATAGATGTGTAAAGATGCTCCTT 535
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 Db 181 TTGTGGAATGCACAGTCATCAAAATTATATAGATGTGTAAAGATGCTCCTT 240
 QY 536 GGGCGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 595
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 Db 241 GGGCGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 300
 QY 596 TTAAACGTGTGGGATATAAAATGAGGTGTCTGCATAGTGAAGAACACATGATCTTGG 655
 |||||
 Db 301 TTAAACGTGTGGGATATAAAATGAGGTGTCTGCATAGTGAAGAACACATGATCTTGG 360
 QY 656 AATTACCTGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 715
 |||||
 Db 361 AATTACCTGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 420
 QY 716 TTTTGCAGTGGCATCATGTGTGTGTCAGATGCGCAAGTCAAAATTTGGATTTTCTTTAC 775
 |||||
 Db 421 TTTTGCAGTGGCATCATGTGTGTGTCAGATGCGCAAGTCAAAATTTGGATTTTCTTTAC 480
 QY 776 CCATATCTTAG 786
 |||||
 Db 481 CCATATCTTAG 491

RESULT 11
 LOCUS B1759505 696 bp mRNA linear EST 25-SEP-2001
 DEFINITION 60304688F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187309 5',
 mRNA sequence.
 ACCESSION B1759505
 VERSION B1759505.1 GI:15751083
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 696)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 plate: LLM11467 row: 0 column: 22
 High quality sequence stop: 696.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:5187309"
 /lab_host="DH10B"
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 /note="Organ: pooled colon, kidney, stomach; Vector:
 PCWV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC library."

ORIGIN

Query Match 38.2%; Score 486.2; DB 4; Length 696;
 Best Local Similarity 99.4%; Pred. No. 9,1e-128;
 Matches 486; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 296 CTCCTCTTCAGACATATTTTGGCATGTGTTCACAGATGTACCACTGTCTATGAA 355
 |||||
 Db 1 CGCTCTGCAGSACATATTTTGGCATGTGTTCACAGATGTGTACCACTGTCTATGAA 60
 QY 356 TACTGAAATGAGACAGATGTGTGCGAGATGAGAACACCTTAGTGGCAGCCCTGAGGGT 415
 |||||
 Db 61 TACTGAAATGAGACAGATGTGTGCGAGATGAGAACACCTTAGTGGCAGCCCTGAGGGT 120
 QY 416 TTGCCAGTTTCCCGCAAGCTCCAAGTGTGGCATGACAGGGCAGCTGATGAACTGTGT 475
 |||||
 Db 121 TTGCCAGTTTCCCGCAAGCTCCAAGTGTGGCATGACAGGGCAGCTGATGAACTGTGT 180
 QY 476 TTGTGGAATGCACAGTCATCAAAATTATATAGATGTGTAAAGATGCTCCTT 535
 |||||
 Db 181 TTGTGGAATGCACAGTCATCAAAATTATATAGATGTGTAAAGATGCTCCTT 240
 QY 536 GGGCGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 595
 |||||
 Db 241 GGGCGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 300
 QY 596 TTAAACGTGTGGGATATAAAATGAGGTGTCTGCATAGTGAAGAACACATGATCTTGG 655
 |||||
 Db 301 TTAAACGTGTGGGATATAAAATGAGGTGTCTGCATAGTGAAGAACACATGATCTTGG 360
 QY 656 AATTACCTGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 715
 |||||
 Db 361 AATTACCTGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTTCATGTGTGA 420
 QY 716 TTTTGCAGTGGCATCATGTGTGTGTCAGATGCGCAAGTCAAAATTTGGATTTTCTTTAC 775
 |||||
 Db 421 TTTTGCAGTGGCATCATGTGTGTGTCAGATGCGCAAGTCAAAATTTGGATTTTCTTTAC 480
 QY 776 CCATATCTTAG 786
 |||||
 Db 481 CCATATCTTAG 491

RESULT 12
 LOCUS AK011391
 DEFINITION Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
 enriched library, clone:2610014F08 product:hypothetical SAM domain
 (sterile alpha motif)/Modified RING finger domain/G-protein beta
 WD-40 repeats containing protein, full insert sequence.
 ACCESSION AK011391
 VERSION AK011391.1 GI:12847483
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 3
 REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K., Fujiwara, S., Inoue, K., Ozawa, Y., Izawa, Y., Ohara, E., Matsui, M., Yoneda, Y., Ishikawa, T., Ogawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL MEDLINE
20530913
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2027)

JOURNAL REFERENCE
AUTHORS
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayashizaki, Y., Hayashizaki, Y., Hiratake, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Izawa, M., Kagawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagami, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL
Submitted (10-JUL-2000) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTVN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAGAGATCTCGAGTTTATTAAATTAATCCCCCCCC 3'. cDNA was cleaved with XhoI and SclI. Cloning sites, 5' end: XhoI; 3' end: SclI.
Host: SOLR.

FEATURES
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166. .1590
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putative"

CDS

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2006. .2011
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polya_site

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75 CTCGACCCCGGACCCCGGAGGAGAGACCCCGGAGCGGAGCTCTCACTCCGAGT
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79 TCCTGAGGCTGTTTCTTCAATAAGACATGATGAACTGATTCACACATTAGCTG
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135 CGAGGAGAGCTGTTTACTTGTGTGAGAGACATGTGATGAGCTGATTCACACCGTGG
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139 ATGATGATGACATGATGACATGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT
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194 ATCAGCGATGATGACGTCAGCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT
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199 TGGACAAACAAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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259 TGAAGTTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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314 TGAAGTTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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319 CATGCTGTTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
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379 CAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
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439 CGTGTGGAGCGCGCGGTGGAGCGCGGTGGAGCGCGGTGGAGCGCGGTGGAGCGCG
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494 CTTACTAGCGTCAAGGCGCGGTGGAGCGCGGTGGAGCGCGGTGGAGCGCGGTGGAGCG
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QY 787 ----- 786
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Db 1511 CTCTCCCTTCACTGTGACTGACCCCAACAGGACATGAAATGAGCCATCAATGATGC 1570
QY 1246 TGGAGACACACCAAAAGTAAA 1266
Db 1571 TGGAGACGACGAGAAAGTAA 1591

RESULT 13
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LOCUS 1700600054632 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN407189
VERSION CN407189.1 GI:47394734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 463)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Gueglis, K., Rao, M.S., Mandilam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R

Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 463 Std Error: 0.00.
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feeder-free conditions"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3,6e-121;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 436 CCACTGTTTGGCATCAGGGGCACTGATGGAACCTGTGTTT 478
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RESULT 14
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LOCUS AL533462/C
DEFINITION AL533462 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
ACCESSION AL533462
VERSION CS0DN004YJ15 3-PRIME, mRNA sequence.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 967)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:12796955.

Contact: Genoscope
Genoscope - Centre National de Sequenage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: sequei@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1653.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DN004CE08NP1&c=1653.r.

FEATURES

source

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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 33.9%; Score 431.4; DB 1; Length 967;
Best Local Similarity 91.3%; Pred. No. 5,4e-112;

Matches 450; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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QY 1194 TCAGCGGTACTTACCAAAATAGGACTCTGAAAATGCGCATCAATAGATGGCTGAGACA 1253
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DB 184 CACCAAAAAGTAAA 172

RESULT 15
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LOCUS

BQ895162 910 bp mRNA linear EST 16-AUG-2002

DEFINITION AGENCOURT 8748888 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6334427

5', mRNA sequence.

ACCESSION BQ895162

VERSION BQ895162.1 GI:22287176

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs@email.nih.gov

Tissue Procurement: Mark Macconochie, Ph.D. and Nancy L. Freeman,
Ph.D.

cDNA Library Preparation: ResGen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLNL13795 row: d column: 12

High quality sequence stop: 601.

Location/Qualifiers

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Job time : 3090 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 05:28:45 ; Search time 178 Seconds
(without alignments)
11692.944 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	45.8	3.6	7218	1	US-08-232-463-14
4	44.8	3.5	1221	3	US-08-965-600-2
5	44.8	3.5	1221	3	US-09-489-506-2
6	43.8	3.4	1141	4	US-09-806-708B-22
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12	40	3.1	246240	2	US-08-724-394A-20
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26	37.4	2.9	29357	4	US-09-949-016-16676
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28	36.8	2.9	1611	3	US-09-302-769-13	Sequence 13, Appl
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31	36.6	2.9	7215	3	US-09-134-001C-627	Sequence 627, Appl
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34	35.8	2.8	389	4	US-09-270-767-26536	Sequence 26536, A
35	35.8	2.8	832	4	US-09-621-976-2813	Sequence 2813, Ap
36	35.8	2.8	899	4	US-09-270-767-11026	Sequence 11026, A
37	35.8	2.8	1743	4	US-09-248-796A-11015	Sequence 11015, A
38	35.6	2.8	1182	4	US-09-248-796A-4568	Sequence 4568, Ap
39	35.6	2.8	4892	4	US-09-976-594-167	Sequence 167, Appl
40	35.6	2.8	5158	4	US-09-023-655-1347	Sequence 1347, Ap
41	35.6	2.8	640681	4	US-09-790-988-1	Sequence 1, Appli
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43	35.4	2.8	2417	4	US-09-254-776B-3	Sequence 3, Appli
44	35.4	2.8	3747	3	US-09-690-364-17	Sequence 17, Appl
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ALIGNMENTS

RESULT 1
US-09-620-312D-768
Sequence 768, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Ruihong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tiliinphast
APPLICANT: Dymnac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PC FL_genes Version 1.0
SEQ ID NO 768
LENGTH: 1844
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (164)..(1594)
US-09-620-312D-768

Query Match 75.8%; Score 964.2; DB 4; Length 1844;
Best Local Similarity 81.8%; Pred. No. 1.9e-307;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

12 TCACCTGGCGGCGACGTCGACCGCGACCGCGCTTGAAGCGGATCCCGCGG 71
65 TCACCTGGCGGCGACGTCGACCGCGACCGCGCTTGAAGCGGATCCCGCGG 124

QY 72 CCCCCTCTGAGGCTGTTTCTTCAATAAAGAACATGTAATCTTACACA 131
DB 125 CCCCCTCTCTGAGGCTGTTTCTTCAATAAAGAACATGTAATCTTACACA 164
QY 132 TTAGCTGATCATGATGATGATGATGATGATGATGATGATGATGATGAT 131
DB 185 TTAGCTGATCATGATGATGATGATGATGATGATGATGATGATGATGAT 244
QY 192 TGCTCTTGGACAAACAAATTCGCTGATGATGATGATGATGATGATGAT 251
DB 245 TGCTCTTGGACAAACAAATTCGCTGATGATGATGATGATGATGATGAT 304
QY 252 TCTCCATTTGAAGTTTCACTTACCTTACCTTACCTTACCTTACCTTAC 311
DB 305 TCTCCATTTGAAGTTTCACTTACCTTACCTTACCTTACCTTACCTTAC 364
QY 312 ATTTTGGCATGCTGTTCAACAGATGATGATGATGATGATGATGATGAT 371
DB 365 ATTTTGGCATGCTGTTCAACAGATGATGATGATGATGATGATGATGAT 424
QY 372 ATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
DB 425 ATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
QY 432 GACTCCACGCTGTTGGCATGAGGGGAGCTGATGAACTGTGTTTGTGAA 491
DB 485 GACTCCACGCTGTTGGCATGAGGGGAGCTGATGAACTGTGTTTGTGAA 544
QY 492 TCATPACAAATTATATAGATGATGATGATGATGATGATGATGATGATGAT 551
DB 545 TCATPACAAATTATATAGATGATGATGATGATGATGATGATGATGATGAT 604
QY 552 TCTCCTAATGGAAGCTTCTTGTCTACAGCTGCTCATGATGATGATGAT 611
DB 605 TCTCCTAATGGAAGCTTCTTGTCTACAGCTGCTCATGATGATGATGAT 664
QY 612 GATPAAAATGAGGTGTCTGATGATGATGATGATGATGATGATGATGAT 671
DB 665 GATPAAAATGAGGTGTCTGATGATGATGATGATGATGATGATGATGAT 724
QY 672 TTTTCTTCAAGCAGCTTCTGATGATGATGATGATGATGATGATGATGAT 731
DB 725 TTTTCTTCAAGCAGCTTCTGATGATGATGATGATGATGATGATGATGAT 784
QY 732 TGTGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
DB 785 TGTGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 844
QY 785 ----- 784
DB 845 GAATPAAAATATATAAGTACATGATGATGATGATGATGATGATGATGAT 904
QY 785 ----- 784
DB 905 TCCCATGATGAGGAGATGATGATGATGATGATGATGATGATGATGAT 964
QY 785 ----- 784
DB 965 ACTAATCTGAGATATACTTCAACATGATGATGATGATGATGATGATGAT 1024
QY 785 ----- 784
DB 1025 GCTTTTGCACCTAATACCTTTTACTGCTACTGCTTCAATGACAAACAGTGA 1084
QY 785 ----- -AGCAAGGGGACAGAACTGAGCTGAAGCAA 815
DB 1085 TGGCAATTTGACCTGGAACAATTGTCACAGCAAGGAGCAACAGCACTGAG 1144
QY 816 TTTACGGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
DB 1145 TTTACGGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1204
QY 876 GATCTTGTGTTGTTTCAAGATGATGATGATGATGATGATGATGATGAT 935

DB 1205 GATCTTGTGTTGTTTCAAGATGATGATGATGATGATGATGATGATGAT 1264
QY 936 AAGAAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 995
DB 1265 AAGAAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1324
QY 996 AGAAATTTGAAGAGCTGAGACCAAGTTAAATCCCTTTCTTCAAGAAAT 1055
DB 1325 AGAAATTTGAAGAGCTGAGACCAAGTTAAATCCCTTTCTTCAAGAAAT 1384
QY 1056 TTTATATGTCATTAATCTAGAGAACTTATGAAAGATCCGTCATGATGAT 1115
DB 1385 TTTATATGTCATTAATCTAGAGAACTTATGAAAGATCCGTCATGATGAT 1444
QY 1116 TCATATGAAAAGGAGACCAATGCAAAATTTGATCAGCAAAAGAAAGCT 1175
DB 1445 TCATATGAAAAGGAGACCAATGCAAAATTTGATCAGCAAAAGAAAGCT 1504
QY 1176 ACAATCTTGTCTTCTTCTTCAAGGATGATGATGATGATGATGATGAT 1235
DB 1505 ACAATCTTGTCTTCTTCTTCAAGGATGATGATGATGATGATGATGAT 1564
QY 1236 AATGATGCTGAGACACACCAAAAGTAA 1266
DB 1565 AATGATGCTGAGACACACCAAAAGTAA 1595

RESULT 2
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHRIJVER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

TELECOMMUNICATION INFORMATION:

```
SOFTWARE: FaastSeq for Windows Version 2.0
```



```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,600
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0416 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 194046
; US-08-965-600-2

```

```

Query Match          3.5%; Score 44.8; DB 3; Length 1221;
Best Local Similarity 49.3%; Pred. No. 0.0011;
Matches 146; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

```

```

QY 328 CAACAGATGTTACCTGCTCTATGGAATCTGAAAATGACAGATGTCGACGTATGG 387
DB 579 CCATAGATGGAATCATCATATTTTATGATGCACTGGAACCTTCGATACCTCG 638
QY 388 AACAGCTATGTCGACGCTCTGAGGGTTGGCCAGTTTCCCAAGTCCACGTGTTGG 447
DB 639 AAGGCC---ATGCCATGCCCATTCGCTCTGACCTTTTCCCGGACTCCGACTCTTG 695
QY 448 CATCAGGGGAGCTGATGAACTGTGTTTGTGGAATGACAGTCAATCAAAATTATATA 507
DB 696 TCACCTGTTGAGATGATGAGCTCACTCAAGATCTATGATGATCAACAGCCAAATTGGCTG 755
QY 508 GATGTGATGTTAAAGATGCTCTCTGGCGCATGTCATTTCTCTTAATGGAAGCT 567
DB 756 GCACGCTGAGCGGCGCATGCTCTCTGGGTGCTGAACGTTGCTGCTGATGACACTC 815
QY 568 TCTTTGCTACTGCTCTCATGTGATTTAAACAGTGGGATGATAAATGAGG 623
DB 816 ACTTTGTTCCAGTTCGCTGACAAAAGTGTAAAGTTGGAGTTGGAACGAGG 871

```

RESULT 5
US-09-489-506-2

```

; Sequence 2, Application US/09489506
; Patent No. 6465619
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW TRANSDUCIN BETA-1 SUBUNIT
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,506
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,600
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0416 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 194046
; US-09-489-506-2

```

```

Query Match          3.5%; Score 44.8; DB 3; Length 1221;
Best Local Similarity 49.3%; Pred. No. 0.0011;
Matches 146; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

```

```

QY 328 CAACAGATGTTACCTGCTCTATGGAATCTGAAAATGACAGATGTCGACGTATGG 387
DB 579 CCATAGATGGAATCATCATATTTTATGATGCACTGGAACCTTCGATACCTCG 638
QY 388 AACAGCTATGTCGACGCTCTGAGGGTTGGCCAGTTTCCCAAGTCCACGTGTTGG 447
DB 639 AAGGCC---ATGCCATGCCCATTCGCTCTGACCTTTTCCCGGACTCCGACTCTTG 695
QY 448 CATCAGGGGAGCTGATGAACTGTGTTTGTGGAATGACAGTCAATCAAAATTATATA 507
DB 696 TCACCTGTTGAGATGATGAGCTCACTCAAGATCTATGATGATCAACAGCCAAATTGGCTG 755
QY 508 GATGTGATGTTAAAGATGCTCTCTGGCGCATGTCATTTCTCTTAATGGAAGCT 567
DB 756 GCACGCTGAGCGGCGCATGCTCTCTGGGTGCTGAACGTTGCTGCTGATGACACTC 815
QY 568 TCTTTGCTACTGCTCTCATGTGATTTAAACAGTGGGATGATAAATGAGG 623
DB 816 ACTTTGTTCCAGTTCGCTGACAAAAGTGTAAAGTTGGAGTTGGAACGAGG 871

```

RESULT 6

```

US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Placenta
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)

```

OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAEI promoters
US-09-806-708B-22

Query Match 3.4%; Score 43.8; DB 4; Length 1141;

Best Local Similarity 9.6%; Pred.No. 0.0023;

Matches 67; Conservative 279; Mismatches 341; Indels 9; Gaps 1;

```

OY 538 CGGATGCGATCTTCTCTAATGAGCTCTTTGTCAGTGGCTCCCATGCTGAT 597
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 53 MSKRKMTWAMTKRWRWNNKSRWNGWYKKWYBPAANTSBKTHARRKDKTAYBM 112
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 598 TAACAGTGGGATGATATAATGAGTGTCTGCATAGTGAATAAGCATGCTGGAA 657
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 113 TMTKMGKTGRHRYWYBAMVDVYDHHYVYAMNNATMTGMDKDRITWMMKKONNA 172
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 658 TTACTGCTGGATTTTCTTCAACAGCCAGTTTGTATGAGAAACAAGCTTCACTTT 717
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 TGMDDTKHYHNNNGCBTVTWVRYKTRDMSBKRNWYGBMWMKMSYDVYVWVWDD 232
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 718 TTGACGCGATCTGCTGATGCGATGCGCAAGTCAAAATTTGATGTTCTTTACC 777
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 233 MCKKXKRWART-----RGRNRYWVAMBTARRRYNNNGTBAVAYRRWNNNNN 283
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 778 ATATCTTAGCAGGCGACAGACATCAGTGAAGCAATTTACGGAATGTGACAGG 837
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 284 NAKAMCKRAKXWGNRBVNSTCTTWKSKTKVATSCANNCRAGDANKHKMKMSAAM 343
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 838 AGTGTCTCAACATGCTGTTGCAACAAGATTTAAAGATCTTGTTGATTTTCAAGA 897
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 344 GYNNNNNNNNNNWYKKARHBAKMDVMVHSAWKKNHANAHSRKMTBYKSKTVNNNG 403
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 898 TGAATTAATGATGAGAAAGAACTGTTGATCTTCAAAAGAAAGCTGCTGATGATT 957
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 404 TTMKRRMAMWKMMDMBGTYNNNNNGRTYTGATKXKKMTYTKMANNCKMRADHK 463
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 958 TGAATTAATGATCTAGAGTGTGTAAGTCTGAGGAATAAGTGAAGCTCAGCA 1017
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 464 TCTNNNTTMMWCKTYNNNCYKSWTNGSHBAAVYVWMMRRVHANNNNMDWYMK 523
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1018 CCAAGTTAAATCCCTTTCTTCAAGAAATCTGATGAATTTATATGTCATAACTGAG 1077
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 524 ACTYKBYVCSKMNWNNYAAWYTKSSWNTSRYYWKTNNNSRWSRDFSRMGRANNYAB 583
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1078 AACTATGAAGAAGATCCGCTATCCATGATGATGCTATTCATATGAAGAAGCAATG 1137
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 584 HYGKMTTRMBWBSHTBHBAGAAHWMWMBYBKCMATKATKAYAGGSSNNNN 643
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1138 AAAATGGATCAGAAAAAGAAAGTACAGTCCCATGCAAAATCTTCTTCTTCCAG 1197
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 644 NNNNNNNNNNNATCARDDYVAAASRWYAMAAKWTYYKBAANNAVYTHANNWGCNNATD 703
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1198 CGTACTTACCACAATAGACTCTGAAATGCGCA 1233
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 704 TRRTWKKNNNNNNAGTWKNNNNNNAKNASAKNYAA 739
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7
US-09-806-708B-22/c

Sequence 22, Application US/09806708B

Patent No. 6784342

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806, 708B

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/147,133

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0

SEQ ID NO 22

LENGTH: 1141

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: Promoter

LOCATION: (1..1141)

OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAEI promoters

US-09-806-708B-22

Query Match 3.4%; Score 43.6; DB 4; Length 1141;

Best Local Similarity 13.2%; Pred.No. 0.0027; Mismatches 309; Indels 5; Gaps 1;

Matches 77; Conservative 192; Mismatches 309; Indels 5; Gaps 1;

```

OY 690 TCTGATGAGAAAGAGCTCTTCAATTTTTCAGTGCATCATGTGCTGAGATGGCAA 749
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1100 TKSATGTAWMTNNAKAGATGCMWYWTGTRNRKCRKTYAMRTYTSNANWSCATBMW 1041
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 750 GTCAAAATTTGATGTTCTTTTACCAATATCTTACCAAGCCGACAGCAATCAGCTG 809
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1040 WTMKCVATKYRTAYAWMCAWRNNNNWCATNGYAKSCATNNAMVYATTRWAAVYAAAKWAR 981
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 810 AAGCAATTTACCAAGATGTGTCAGAGAGTGTCTCAACATGCTTGTGCAAGAT 869
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 980 WAGNNMRYGAAAGNKKGCMAAAATGCBWADTAGKVCNNNNNNWTTDVERMAHAKANN 921
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 870 TTAAGAATCTTGTGTATTTCAAGATGATPAATGATGAGAAAGAACTGTTGAT 929
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 920 NNNAYWTACYNRAATNNKATHTHMKWTHGAHSKRTHHRTCRRTKYNNNNNARTVW 861
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 930 CTTAACAAAGAAAGCTGCGTATGATTTGAAAATTTGAATCTTACAGTCCGTAGTAA 989
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 860 YHHAARRMMAWMTRTNNNNNNNNNNNACRNTRTWABMKHSWCNNNNNNNNNNNTWC 801
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 990 GTGTGAGAAATTTGAAGCTCAGACCAAGTTAAATCCCTTCTTCAAGAACTCT 1049
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 800 HYTANABBCYRANNNNAARMARTCNVYAAATTTHTWCKYTWNTWYDMMTWTBT 741
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1050 GATGAATTTATGATCCAAATACAGAGAACTTATGAAGATCCGCTATGCTCAGAT 1109
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 740 TTRNNMTTSTNNNNNNNNNNNNWACCTNNNNNNMMKAYVHAATNNCCW-----NTDART 686
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1110 GCGTATTCATGAGAAAGAAAGCAATGAGAAATTTGATCAGCAAAAGAAAGTACAGT 1169
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 685 NNTVMRRMMWMTYKTYWSTTRRHHTGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 626
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1170 CCATGCAAAATCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1229
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 625 TMDGDTVRKRWRTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 566
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1230 GCCATCAATGATGCGCTGAGACACACCAAGTAAAGATTC 1272
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 565 YMSNNMWMYRRYSARRNSSMARWTTTRNNWMSGBVRWRMAGTM 523
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 8
US-10-101-464A-251

Sequence 251, Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020C2

CURRENT APPLICATION NUMBER: US/10/101, 464A

PRIOR FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228, 986

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162, 866

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR FILING DATE: 2000-01-11

```

: NUMBER OF SEQ ID NOS: 989
: SOFTWARE: SeqSeq for Windows Version 4.0
: SEQ ID NO: 251
: LENGTH: 937
: TYPE: DNA
: ORGANISM: Eucalyptus grandis
: US-10-101-464A-251

```

Query Match	3.4%	Score 43;	DB 4;	Length 937;
Best Local Similarity	51.9%	Pred. No. 0.0037;		
Matches	97;	Conservative	0;	Mismatches 90;
				Indels 0;
				Gaps 0;

QY	1060	TATGTCCAAATACATAGAGACTTATGAAAGATCCGGTATCGCATCGATGGCATTTTCAT	1119
Db	732	TGTGCCCATCTCTTCAGGAAATATGATGATCCTCAGATTGCGCGGATGGTTTCACTT	791
QY	1120	ATGAAAAGGAGCAATGGAATTTGGATTCAGCAAAAAGAAACGTTCMAAGTCCCATGACAA	1179
Db	792	ATGAAGGAGAGCTATCGGGGATGGTTTGGACAAAGACACAGATATCAATCGGCATGACAA	851
QY	1180	ATCTTTTCTTCCCTTCAGCGGACTTACACAAATAGCACTCTGAAAAATGGCCATCAATA	1239
Db	852	ACTTGAACTTAGTCAATTGCACTTCACCTCCCAACACGCGTTACGTCGGGAATTCAG	911

Qy	1240	GATGGCT	1246
Db	912	AGTGGCT	918

RESULT 9
US-09-345-882-1/c

; faceit no: 8399573
; GENERAL INFORMATION:
; APPLICANT: Boucraoui

FILE REFERENCE: GENSET.031A

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)

TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

```

CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1

```

```

; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:

```

```

; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C

```

```

; NAME/KEY: allcle
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or

```

```

; RECORD:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT

```

```

; FEATURE:
; NAME/KEY: al1e1e
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : no polymorphic base G or T

```

```

; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
;

```

OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T

NAME/KEY: a11e1e
LOCATION: 99098

OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele

OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:

LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T

NAME/KEY: allele
LOCATION: 106940

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FEATURE: 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99
NAME/KEY: allele

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OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:

LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTTT

NAME/KEY: a1e1e
LOCATION: 108308

FEATURE:
NAME/KEY: allele

OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:

LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T

NAME/KEY: allele
LOCATION: 134362

NAME/KEY:	allele
FEATURE:	
CHROM. INFORMATION:	3-170-370
	polymorphic base
	insersion

OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:

NAME/ALI: 81818
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G

FEEDINGS:
 NAME/KEY: allele
 LOCATION: 146345

OTHER INFORMATION:	3-143-101	POLYMORPHIC	BASE	N	01
FEATURE:					
NAME/KEY:	a1e1e				

LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:

NAME/NEI: alicia
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T

FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817

OTHER INFORMATION: POLYMERASE CHAIN REACTION (PCR) ANALYSIS OF THE DNA SAMPLES FROM THE VICTIM AND THE SUSPECTS. THE RESULTS SHOWED THAT THE DNA FROM THE SUSPECTS MATCHED THE DNA FROM THE VICTIM. THE RESULTS WERE CONFIRMED BY AN INDEPENDENT LABORATORY.

LOCATION: 12/11..1281/
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:

NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31

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NAME/KEY allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

Query Match 3.2%; Score 40.4; DB 3; Length 162450;
Best Local Similarity 52.4%; Pred. No. 1;
Matches 89; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1021 AGGTAAATCCCTCTCTTCAGGAATCCGATGATATTTATGATCCATAATACAGAGAAC 1080
DB 73713 AGGAGAAATATATTTTAACTGAGAGTAGTAACAGTTAATATTCACAAATATATTAAGAAC 73655
QY 1081 TTATGAAAGATCCGTCATCGCATCGATGCGCTATTCATATGATGAAAAGAACATVGGAA 1140
DB 73653 ACATATATCCAAACCTAATAAGAAAAGATATAATCATCTCAAGAGAAAAGCGAAACATAT 73599
QY 1141 ATTGGATCAGCAAAAAGAAACGTACAGTCCCATGACAAATCTGTTCCT 1190
DB 73593 AAGAGCCAGCAACTCAAAAACGAGAAAACACAAATGATATATGTTCCT 73544

RESULT 10
US-08-188-582-17
Sequence 17, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ. ID NO.: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pairs

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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2112
US-08-188-582-17

Query Match 3.1%; Score 40; DB 1; Length 2152;
Best Local Similarity 48.3%; Pred. No. 0.065;
Matches 112; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 407 TGTGAGGCTTTGCCAGTTTCCCGACATCCAGCTGTTGGCATCAGGGGACCTGATGG 466
DB 1599 TGTGAATTGTACAGATTCATCCAAATTATATATGTTGCTACAGGGCTCTGACAGAC 1658
QY 467 AACTGTGTTTGTGGAATGACAGTCATCAAAATTATATATAGATGTGTAGTTAAAG 526
DB 1659 AACTGTGCGGCTCTGGAGAGCTCTGAATGTTAATGTTAAGATCTTCACTGGACACA 1718
QY 527 TGGCTCTTGGCGGCATGTGCATTTTCTCTATATGAAAGCTTTTGTCACTGGCTCTC 586
DB 1719 GGGACCAATTCAATCTCTTGACATTTTCTCCCAATGGAGATTCCTGGCTACAGAGCAAC 1778
QY 587 ATGTGCTGATTTTAACAGTGTGGATGATAAATGAGGTCTGCATAGTGA 638
DB 1779 AGATGGCAGAGTCTCTTGGGATATGACATGTTGATGTGTGAGAA 1830

RESULT 11
US-08-646-715-17

Sequence 17, Application US/08646715

Patent No. 5637686

GENERAL INFORMATION:

APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Wozniak, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
NUMBER OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
CORRESPONDENCE ADDRESS: 36
ADDRESS: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,715

FILING DATE: 09-MAY-1996

CLASSIFICATION: 435

Prior Application DATA:

APPLICATION NUMBER: US 08/188,582

FILING DATE: 28-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2112
US-08-646-715-17

Query Match 3.1%; Score 40; DB 1; Length 2152;
Best Local Similarity 48.3%; Pred. No. 0.065;
Matches 112; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 407 TGTGAGGCTTTGCCAGTTTCCCGACATCCAGCTGTTGGCATCAGGGGACCTGATGG 466
DB 1599 TGTGAATTGTACAGATTCATCCAAATTATATATGTTGCTACAGGGCTCTGACAGAC 1658
QY 467 AACTGTGTTTGTGGAATGACAGTCATCAAAATTATATAGATGTGTAGTTAAAG 526
DB 1659 AACTGTGCGGCTCTGGAGAGCTCTGAATGTTAATGTTAAGATCTTCACTGGACACA 1718
QY 527 TGGCTCTTGGCGGCATGTGCATTTTCTCTATATGAAAGCTTTTGTCACTGGCTCTC 586
DB 1719 GGGACCAATTCAATCTCTTGACATTTTCTCCCAATGGAGATTCCTGGCTACAGAGCAAC 1778
QY 587 ATGTGCTGATTTTAACAGTGTGGATGATAAATGAGGTCTGCATAGTGA 638
DB 1779 AGATGGCAGAGTCTCTTGGGATATGACATGTTGATGTGTGAGAA 1830

RESULT 12
US-08-724-394A-20

Sequence 20, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map. No. 5872237e1
NUMBER OF INVENTION: Sequences and Antibodies Thereof
CORRESPONDENCE ADDRESS: 31
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Filts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match 3.1%; Score 40; DB 2; Length 246240;
Best Local Similarity 55.9%; Pred. No. 1.9;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 773 TACCATATCTTAGCAGAGCGCACAGAACATCAGTGAAGCAATTTACCGAAGATTGTC 832
DB 45039 TACTCATGCTGATGAATTTACCAAAACATACCCCTGGGCCAATTAACAAACAGCAGAGC 45098
QY 833 AAGAGAGTCGTCTCAACATGCGTTTGTGCACAAGATTAAAGATCTTGTGATTTT 892
DB 45099 AAATGTTGTGTGTGTATTAACCTTCTACCAAAATACGAAAAAAGTGAATTCATGTT 45158
QY 893 CAAGATGAATTAACATT 908
DB 45159 CAGCATTAATTAATTT 45174

RESULT 13
US-08-724-394A-21
Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereo
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

Query Match 3.1%; Score 40; DB 2; Length 246240;
Best Local Similarity 55.9%; Pred. No. 1.9;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 773 TACCATATCTTAGCAGAGCGCACAGAACATCAGTGAAGCAATTTACCGAAGATTGTC 832
DB 45039 TACTCATGCTGATGAATTTACCAAAACATACCCCTGGGCCAATTAACAAACAGCAGAGC 45098
QY 833 AAGAGAGTCGTCTCAACATGCGTTTGTGCACAAGATTAAAGATCTTGTGATTTT 892
DB 45099 AAATGTTGTGTGTGTATTAACCTTCTACCAAAATACGAAAAAAGTGAATTCATGTT 45158
QY 893 CAAGATGAATTAACATT 908
DB 45159 CAGCATTAATTAATTT 45174

RESULT 14
US-08-724-394A-22
Sequence 22, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereo
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

Query Match	3.1%	Score 40;	DB 2;	Length 246240;
Best Local Similarity	55.9%;	Pred. No. 1.9;		
Matches 76;	Conservative 0;	Mismatches 60;	Indels 0;	Gaps 0;

QY	773	TACCCATATATTTCGACAGGGGACAGAACATCAGCTGAGCAATTTACCGAATGTCG	832
Db	45039	TACTCATGCTGATGAGATTTACCAAACTACCTCGGGCCATTAACAAAGCAGGAGC	450988
QY	833	AGAGAGAGTCGCTCAACATGCGCTTTGTGCACAGATTTAAAAGATCTGTGGTATTT	892
Db	45099	AAATGCTTTGTGTGTATTAACCTTCTACACAAATTAAGAAAAAGTGAATTCATGTT	451588
QY	893	CAAGATCAATTAACATT	908
Db	45159	CAGCATTAATTAATTT	45174

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RESULT 15
US-09-690-364-10
; Sequence 10, Application US/09690364
; Patent No. 6468795
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF APAF-1 EXPRESSION
; FILE REFERENCE: RTS-0150
; CURRENT APPLICATION NUMBER: US/09/690,364
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 10
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (386)...(4302)
; US-09-690-364-10

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Query Match	3.1%;	Score 39.6;	DB 3;	Length 5152;
Best Local Similarity	54.9%;	Pred. No. 0.16;		
Matches 78;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;

QY	442	GTTTGCATAGGGGGACGTCGATGGAACGTGCGTTTGTGGAATGCACAGCATACAAAT	501
QY	3722	GATTGCTTTCTTGGTCATTGATGTAACCGGTGAAGTGTGGAATGTCATACCGGAAGAA	3781
Db	502	TATATAGATGNGTAGTGTAAAGATGGCTCCTTGGGGGCATGTGCATTTCTCCTATG	561
QY	3782	TAGAAAGACATTACTTGTATATAGGGGACAGTGTCTTCTGTGTAATCTTCTGTAGT	3841
Db	562	GAAGCTTCTTGTCACTGGCTC	583
QY	3842	CGACCAAGTTTCTCTTACTCTC	3863
Db			

Search completed: October 25, 2005, 07:46:32
Job time : 185 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 06:52:11 : Search time 2669 Seconds
(without alignments)
3933.065 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272

Sequence: 1 gaattcggttcctaccctgcg.....acaccataagtaagaattc 1272

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9772377 seqs, 4126317084 residues

Total number of hits satisfying chosen parameters: 19544754

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1272	100.0	1272	14	US-10-077-111-12 Sequence 12, Appl
2	977.2	76.8	1553	14	US-10-077-111-3 Sequence 3, Appl
3	965.8	75.9	1818	14	US-10-077-111-1 Sequence 1, Appl
4	964.2	75.8	1817	10	US-09-971-392-207 Sequence 207, App
5	964.2	75.8	1821	22	US-10-956-157-5128 Sequence 5128, Ap

6	964.2	75.8	1844	16	US-10-037-270-768 Sequence 768, App
7	964.2	75.8	1844	18	US-10-117-722-768 Sequence 768, App
8	894	70.3	1773	17	US-10-287-218-40 Sequence 40, Appl
9	894	70.3	1773	20	US-10-474-291-40 Sequence 40, Appl
10	890.2	70.0	1811	18	US-10-104-047-1689 Sequence 1689, Ap
11	878.8	69.1	1996	21	US-10-357-930-23179 Sequence 23179, A
12	878.8	69.1	1996	21	US-10-357-930-29046 Sequence 29046, A
13	877.8	69.0	1908	14	US-10-077-111-14 Sequence 14, Appl
14	602.2	47.3	1400	22	US-10-956-157-10563 Sequence 10563, A
15	464	36.5	1901	14	US-10-077-111-6 Sequence 6, Appl
16	377.2	29.7	630	14	US-10-077-111-5 Sequence 5, Appl
17	335	26.3	446	21	US-10-357-930-5029 Sequence 5029, Ap
18	331.6	26.1	366	9	US-09-864-761-10657 Sequence 10657, Ap
19	329.8	25.9	409	21	US-10-357-930-14198 Sequence 14198, A
20	328.8	25.8	441	21	US-10-357-930-35319 Sequence 35319, A
21	328.8	25.8	441	21	US-10-357-930-44154 Sequence 44154, A
22	297	23.3	297	9	US-09-864-761-27306 Sequence 27306, A
23	291.6	22.9	419	24	US-10-779-543-8962 Sequence 8962, Ap
24	179.6	14.1	466	9	US-09-864-761-11052 Sequence 11052, A
25	176.8	13.9	180	9	US-09-864-761-27687 Sequence 27687, A
26	154	12.1	520	14	US-10-077-111-8 Sequence 8, Appl
27	146.6	11.5	399	24	US-10-779-543-12137 Sequence 12137, A
28	142.6	11.2	480	9	US-09-864-761-13978 Sequence 13978, A
29	132	10.4	132	9	US-09-864-761-30542 Sequence 30542, A
30	129.4	10.2	604	13	US-09-925-065A-667748 Sequence 667748, A
31	129.4	10.2	604	13	US-09-925-065A-667749 Sequence 667749, A
32	129.4	10.2	604	13	US-09-925-065A-667750 Sequence 667750, A
33	129.4	10.2	604	13	US-09-925-065A-667751 Sequence 667751, A
34	129.4	10.2	604	13	US-09-925-065A-667752 Sequence 667752, A
35	118.2	9.3	478	10	US-09-918-995-13423 Sequence 13423, A
36	92	7.2	428	14	US-10-027-632-62257 Sequence 62257, A
37	92	7.2	428	14	US-10-027-632-62257 Sequence 62257, A
38	91	7.2	428	14	US-10-027-632-35838 Sequence 35838, A
39	91	7.2	428	14	US-10-027-632-35838 Sequence 35838, A
40	87	6.8	92	16	US-10-106-698-3381 Sequence 3381, Ap
41	76	6.0	439	14	US-10-027-632-195937 Sequence 195937, A
42	76	6.0	439	18	US-10-027-632-195937 Sequence 195937, A
43	70	5.5	573	13	US-09-925-065A-736064 Sequence 736064, A
44	62.8	4.9	2511	18	US-10-260-238-549 Sequence 549, App
45	62.8	4.9	2813	20	US-10-437-963-64112 Sequence 64112, A

ALIGNMENTS

RESULT 1
US-10-077-111-12
Sequence 12, Application US/10077111
Publication No. US20020187492A1
GENERAL INFORMATION:
APPLICANT: Toddard, C. Gordon
APPLICANT: Finger, Joshua N.
APPLICANT: Rillema, Jill
TITLE OF INVENTION: TBA
FILE REFERENCE: 3053-4114US2
CURRENT APPLICATION NUMBER: US/10/077, 111
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/294,181
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/269,366
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1272
TYPE: DNA
ORGANISM: HUMAN
FEATURES:
OTHER INFORMATION: RET 16.2 splice variant
US-10-077-111-12
Query Match 100.0%; Score 1272; DB 14; Length 1272;
Best Local Similarity 100.0%; Pred. No. 0;

QY 421 AGTTTCCCGAGACTGCGGTTTGGCATCAGGGGAGCGATGAACTGTGGTTTGT 480
DB 421 AGTTTCCCGAGACTGCGGTTTGGCATCAGGGGAGCGATGAACTGTGGTTTGT 480
QY 481 GGAATGACAGTACATCAAAATTATATAGATGTGTAGTTAAAGATGGCTCTTGGCGG 540
DB 481 GGAATGACAGTACATCAAAATTATATAGATGTGTAGTTAAAGATGGCTCTTGGCGG 540
QY 541 CAGTGTGATTTTCTCCATGGAAGCTTTCTTGTCACTGGCTCTCATGTGGTATTTAA 600
DB 541 CAGTGTGATTTTCTCCATGGAAGCTTTCTTGTCACTGGCTCTCATGTGGTATTTAA 600
QY 601 CAGTGTGGAATGAAATGAGGTCTGATAGTGAAGAAAGCAATGCTTGAATTA 660
DB 601 CAGTGTGGAATGAAATGAGGTCTGATAGTGAAGAAAGCAATGCTTGAATTA 660
QY 661 CCGCTGCGATTTTCTTCAAGCCAGTTTCTGATGAGAAACAAGTCTTCAATTTTTC 720
DB 661 CCGCTGCGATTTTCTTCAAGCCAGTTTCTGATGAGAAACAAGTCTTCAATTTTTC 720
QY 721 GACTGGCATCATGTGTGATGAGATGCGCAAGTCAAAATTTGGATTGTTTCCCATTA 780
DB 721 GACTGGCATCATGTGTGATGAGATGCGCAAGTCAAAATTTGGATTGTTTCCCATTA 780
QY 781 TCTTT----- 784
DB 781 TCTTTAGGTTTGAATTAATAATAAAGTACACTGATGGGCACTGTCTCTGTTCTGG 840
QY 785 ----- 784
DB 841 CTTGTGCTTTTCCCGTATGCGGAGATGCTAGTCTCAGGGTCACTGATGATTAAGTCTGCA 900
QY 785 ----- 784
DB 901 TAGATATGATATAATACTAGAAATATCTTCAACATTTGACTCAGACACAGATATG 960
QY 785 ----- 784
DB 961 TCACAACTTGCTTTTGGACCTTAATACCTTTTACTTGCTACTGTTCAATGAGACAAA 1020
QY 785 ----- AGCAAGCGCAGACAAATC 804
DB 1021 CAGTGAACATCTGGCAATTTGACCTGGAAACACTTTGCCAAGCAGGCGCAGAAATC 1080
QY 805 AGCTGAAGCAATTTTACCGAAGATTGTCAGAGAGGTGCTCAACATGGCTTTGTGCAC 864
DB 1081 AGCTGAAGCAATTTTACCGAAGATTGTCAGAGAGGTGCTCAACATGGCTTTGTGCAC 1140
QY 865 AAGATTTAAAAGATCTTGTGTGATTTTCAAGATGAATAACATGATGGAAGAAACATCT 924
DB 1141 AAGATTTAAAAGATCTTGTGTGATTTTCAAGATGAATAACATGATGGAAGAAACATCT 1200
QY 925 TGAATCTTACAAAGAAAGTCTGCTGATGATTTGAAATGAAATCTCTAGGACTGGCTA 984
DB 1201 TGAATCTTACAAAGAAAGTCTGCTGATGATTTGAAATGAAATCTCTAGGACTGGCTA 1260
QY 985 GTAAAGTCTGAGGAAATTTGAAAGCTCAGAGCAAGTTAAATCCCTTTCTTCAAGAA 1044
DB 1261 GTAAAGTCTGAGGAAATTTGAAAGCTCAGAGCAAGTTAAATCCCTTTCTTCAAGAA 1320
QY 1045 TTCTCTGATGATTTTATATGTCCAACTAAGAACTTAAGAAATCCGCTCATCCGAT 1104
DB 1321 TTCTCTGATGATTTTATATGTCCAACTAAGAACTTAAGAAATCCGCTCATCCGAT 1380
QY 1105 CAGATGCTATTTCAATGAAAGAAAGCAATGAAATTTGGATCAGCAAAAGAAACGTA 1164
DB 1381 CAGATGCTATTTCAATGAAAGAAAGCAATGAAATTTGGATCAGCAAAAGAAACGTA 1440
QY 1165 CAAATGCCATGACAAATCTTGTCTTCTTCAAGCGGATCTTCAACCAATTAAGACTCTGA 1224
DB 1441 CAAATGCCATGACAAATCTTGTCTTCTTCAAGCGGATCTTCAACCAATTAAGACTCTGA 1500

QY 1225 AATGGCCATCAATAGATGCTGGAGACACACCAAAAGTAAGA 1268
DB 1501 AATGGCCATCAATAGATGCTGGAGACACACCAAAAGTAAGA 1544

RESULT 3
US-10-077-111-1
; Sequence 1, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Toddlerud, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-4114US2
; CURRENT APPLICATION NUMBER: US/10/077,111
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: HUMAN
US-10-077-111-1

Query Match 75.9%; Score 965.8; DB 14; Length 1818;
Best Local Similarity 81.8%; Pred. No. 9.1e-271;
Matches 1253; Conservative 0; Mismatches 2; Indels 276; Gaps 1;

QY 12 TCACCTGCGGCGACGTGACCCGACCCCGTGGGCACTTGAAGCGATCCGCGG 71
DB 49 TCACCTGCGGCGACGTGACCCGACCCCGTGGGCACTTGAAGCGATCCGCGG 108
QY 72 CCCCCGCTCGACAGGCTGTTTCTTCAATAAAGAAACAGTGAATTCACACA 131
DB 109 CCCCCGCTCGACAGGCTGTTTCTTCAATAAAGAAACAGTGAATTCACACA 168
QY 132 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
DB 169 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 228
QY 192 TGCTCTTGAACAACAATTCGCTGATCTGTTACGTGATCTTGAATGATGATGAT 251
DB 229 TGCTCTTGAACAACAATTCGCTGATCTGTTACGTGATCTTGAATGATGATGAT 288
QY 252 TCTCCATTTGAAGTTTCACTATGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCT 311
DB 289 TCTCCATTTGAAGTTTCACTATGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCT 348
QY 312 ATTTTGGATCGTGTTCACAGATGTAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
DB 349 ATTTTGGATCGTGTTCACAGATGTAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
QY 372 ATGTGCACTGATGTAACAGCTAGTGGAGCCCTGTGAGGGTTTCCAGTTTCCCA 431
DB 409 ATGTGCACTGATGTAACAGCTAGTGGAGCCCTGTGAGGGTTTCCAGTTTCCCA 468
QY 432 GACTCCACGTGTTTGGATCAAGGGGCACTGATGGAACCTGTGTTTGTGGAATGCAAG 491
DB 469 GACTCCACGTGTTTGGATCAAGGGGCACTGATGGAACCTGTGTTTGTGGAATGCAAG 528
QY 492 TCATACAAATTAATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
DB 529 TCATACAAATTAATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
QY 552 TCTCTTAATGAAGCTTCTTGTCACTGGCTCTCATGTGTGATTTAAACAGTGTGGAT 611
DB 589 TCTCTTAATGAAGCTTCTTGTCACTGGCTCTCATGTGTGATTTAAACAGTGTGGAT 648

QY	612	GATAAATAGAGTGTCTGATAGTGAAGAAACACATGATCTTGAATTAACCTGCTGCAT	671
Db	649	GATAAATAGAGTGTCTGATAGTGAAGAAACACATGATCTTGAATTAACCTGCTGCAT	708
QY	672	TTTTCTTCACAGCCAGTTCATGATGAGAAAGGCTCTTCAGTTTTCGACTGGCATCA	731
Db	709	TTTTCTTCACAGCCAGTTCATGATGAGAAACAGGCTTCAGTTTTCGACTGGCATCA	768
QY	732	TGTGTCACGAGTTGGCAGTCAGAAATTTGGATTTGTTCTTTTACCATATCTT-----	784
Db	769	TGTGTCACGAGTTGGCAGTCAGAAATTTGGATTTGTTCTTTTACCATATCTTAGTTT	828
QY	785	-----	784
Db	829	GAAATTAATAATATAAGTACACTGAGTGGGACCTGTCTCCTGTTCTGCTTGCTTTT	888
QY	785	-----	784
Db	889	TCCCATGATGGGACAGATGCTAGTCTCAGGGTCAGTGAATGATCTGTATAGTATGAT	948
QY	785	-----	784
Db	949	ACTAATACTGAAATATATCTTCACACTTGACTCAGACACACAGTATGTCACACTTGT	1008
QY	785	-----	784
Db	1009	GCTTTGCACCTAATATACCTTTTACTTCTACTGTCTCAATGACAAATACGTGAACATC	1068
QY	785	-----ACGAGGCGCAGACGAAACATCAGCTGAGCA	815
Db	1069	TGGCAATTTGACCTGGAAACATTTGGCAAGAGGGCCACGAAACATCAGCTGAAGCA	1128
QY	816	TTTACCGAAGATTGGTCAAGAGAGTGGTCTCAACATGGCTTTGTGCAAGATTTAA	875
Db	1129	TTTACCGAAGATTGGTCAAGAGAGTGGTCTCAACATGGCTTTGTGCAAGATTTAA	1188
QY	876	GATCTGTGGATTTTCAAGATGAATAACATGATGGAAGAAACGTGAACTTCA	935
Db	1189	GATCTGTGGATTTTCAAGATGAATAACATGATGGAAGAAACGTGAACTTCA	1248
QY	936	AAAGAAAGTCTGGCTGATGATTTGAAATTTGAATCTTACGAGCTGCGTAAAGTGGT	995
Db	1249	AAAGAAAGTCTGGCTGATGATTTGAAATTTGAATCTTACGAGCTGCGTAAAGTGGT	1308
QY	996	AGGAAATTTGAAGCTCAGACCCAAAGTTAAATCCCTTTCACAGAAATTCGTAGAA	1055
Db	1309	AGGAAATTTGAAGCTCAGACCCAAAGTTAAATCCCTTTCACAGAAATTCGTAGAA	1368
QY	1056	TTTATATCTCCAAATACCTAGAACTTTATGAAAGTCCGGTCACTGATGATGGCTAT	1115
Db	1369	TTTATATCTCCAAATACCTAGAACTTTATGAAAGTCCGGTCACTGATGATGGCTAT	1428
QY	1116	TCATATGAAAGAAAGCAATGGAATTTGATTCAGCAAAAAGAAACGTACAGTCCCATG	1175
Db	1429	TCATATGAAAGAAAGCAATGGAATTTGATTCAGCAAAAAGAAACGTACAGTCCCATG	1488
QY	1176	ACAAATCTTGTCTTCTTCACGCGTACTTACACCAATATGAGCTCTGAAATGGCCATC	1235
Db	1489	ACAAATCTTGTCTTCTTCACGCGTACTTACACCAATATGAGCTCTGAAATGGCCATC	1548
QY	1236	AATAGATGGCTGGAGACACACCAAAAGTAA	1266
Db	1549	AATAGATGGCTGGAGACACACCAAAAGTAA	1579

RESULT
US-09-971-392-207
Sequence 207, Application US/099713922
Publication No. US20030134283A1
GENERAL INFORMATION:
APPLICANT: Peterson, David P.
APPLICANT: Pearson, Cecilia I.
APPLICANT: Cocks, Benjamin G.

```

; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
;
; FILE REFERENCE: PA-0029 US
;
; CURRENT APPLICATION NUMBER: US/09/971,392
;
; CURRENT FILING DATE: 2001-10-03
;
; PRIOR APPLICATION NUMBER: 60/237,652
;
; PRIOR FILING DATE: 2000-10-03
;
; NUMBER OF SEQ ID NOS: 260
;
; SOFTWARE: PERL Program
;
; SEQ ID NO 207
;
; LENGTH: 1817
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: misc feature
;
; OTHER INFORMATION: Template ID: 158923.9
;
US-09-971-392-207

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Query Match	75.8%	Score 964.2	DB 10	Length 1817
Best Local Similarity	81.8%	Pred. NO. 2.7e-270		
Matches 1252	Conservative	0	Mismatches 3	Indels 276
				Gaps 1

QY	12	TCACCTGGGGGACGTACCCCGACCCGCGGTGGGACCTTGAAGGGGATCCCGGGG	71
Db	49	TCACCTGGGGGACGTACCCCGACCCGCGGTGGGACCTTGAAGGGGATCCCGGGC	108
QY	72	CCCCGCGCTCTGCAGGCTGTTTTCTTCAATTAAGAACATGGTGAACCTGATTCCACA	131
Db	109	CCCCGCGCTCTGCAGGCTGTTTTCTTCAATTAAGAACATGGTGAACCTGATTCCACA	168
QY	132	TTAGCTGATCATGTGACGATGTCAACTGTGTGCTTCTCCTTTTCCCTCTTGGCTACT	191
Db	169	TTAGCTGATCATGTGACGATGTCAACTGTGTGCTTCTCCTTTTCCCTCTTGGCTACT	228
QY	192	TGCTCCCTTGGACAAAACAATTGGCCGTGATCTACGTATACGGACTTTATCTGAATCGGCACAT	251
Db	229	TGCTCCTTGGACAAAACAATTGGCCGTGATCTGTAACGTACTTTATCTGAATCGGCACAT	288
QY	252	TCTCCATTGAAGTTTCATACCTATGCTGTGCACCTGCTGTGTTCTCCCTTCAGGACAT	311
Db	289	TCTCCATTGAAGTTTCATACCTATGCTGTGCACCTGCTGTGTTCTCCCTTCAGGACAT	348
QY	312	ATTTTGGCATGTGTTCACAACAGATGGTACCACTGTCTCTATGGAATATCTGAATAATGACACAG	371
Db	349	ATTTTGGCATGTGTTCACAACAGATGGTACCACTGTCTCTATGGAATATCTGAATAATGACACAG	408
QY	372	ATGCGGAGATGATGGAAACAGCTATGTGGACGCCCTGTGAGGGTTTGGCAGTTTCCCA	431
Db	409	ATGCGGAGATGATGGAAACAGCTATGTGGACGCCCTGTGAGGGTTTGGCAGTTTCCCA	468
QY	432	GACTTCACGTTGTTGGCATACAGGGGACAGCTGATGGAACGTGTGGTTTTGTGGAATGCACAG	491
Db	469	GACTTCACGTTGTTGGCATACAGGGGACAGCTGATGGAACGTGTGGTTTTGTGGAATGCACAG	528
QY	492	TCATACAAATTATATAGATGTGTGATGTTTAAAGATGAGCTCCTTGGCGGACATGTGCAATT	551
Db	529	TCATACAAATTATATAGATGTGTGATGTTTAAAGATGAGCTCCTTGGCGGACATGTGCAATT	588
QY	552	TCTCCTAATGGAAGCTTCTTTGTCACTGGCTCCTCATGTGGATGATTTAACAGGTGGGAT	611
Db	589	TCTCCTAATGGAAGCTTCTTTGTCACTGGCTCCTCATGTGGATGATTTAACAGGTGGGAT	648
QY	612	GATAAAATGAGGTGTCTGCATAGTAAATAAGACACATGATCTTGGAAATTAACCTGCTCGCAT	671
Db	649	GATAAAATGAGGTGTCTGCATAGTAAATAAGACACATGATCTTGGAAATTAACCTGCTCGCAT	708
QY	672	TTTTCTTCAACGCCAGTTTCTGATGTGAAGAACAAAGCTCTTCAAGTTTTTGCACGTGCAATCA	731
Db	709	TTTTCTTCAACGCCAGTTTCTGATGTGAAGAACAAAGCTCTTCAAGTTTTTGCACGTGCAATCA	768
QY	732	TGTGTCAGGATTCGCAAGTCAAAATTTTGGATGTTTCTTTTAACCATATCTT-----	784
Db	769	TGTGTCAGGATTCGCAAGTCAAAATTTTGGATGTTTCTTTTAACCATATCTTAAGGTTTTT	828

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Qy 785 ----- 784
Db 829 GAATTAATAATAAGTACAGTGAAGGACCTGCTCTCTGTTCTGGCTTGCTTT 888
Qy 785 ----- 784
Db 889 TCCCATGATGGGAGATGCTAGTCTCAGGGTCAAGTGATAAGTCTCATATATATGAT 948
Qy 785 ----- 784
Db 949 ACTAATACTGAGAAATATACTTCAACATTGACTCAGACACAGATATGTCACAACCTGT 1008
Qy 785 ----- 784
Db 1009 GCTTTGACCTAATAACCTTTTACTTGCTAGTCTGTTCAATGACAAAGACATGACATC 1068
Qy 785 ----- -AGCAAGGCGCACAGAACATCAGCTGAACCAA 815
Db 1069 TGGCAATTGACCTGGAACACTTTGGCCAAAGAGACAGAACATCAGCTGAACCAA 1128
Qy 816 TTTACCGAAGATGCTGAGAGAGAGTGTCTCAACATGGCTTTGTGACAAAGATTTTAAA 875
Db 1129 TTTACCGAAGATGCTGAGAGAGAGTGTCTCAACATGGCTTTGTGACAAAGATTTTAAA 1188
Qy 876 GATCTTGTGTATTTTCAAGATGATATACATTGATGAAAAAGAACTGTTGAATCTTACA 935
Db 1189 GATCTTGTGTATTTTCAAGATGATATACATTGATGAAAAAGAACTGTTGAATCTTACA 1248
Qy 936 AAAAGAAAGTGTGCTGATGATTTGAAAAATTGAATCTGAGACTGCTAGTAAAGTCTG 995
Db 1249 AAAAGAAAGTGTGCTGATGATTTGAAAAATTGAATCTGAGACTGCTAGTAAAGTCTG 1308
Qy 996 AGCAAAATTTGAAGCTCAGACCAAGGTTAAATCCCTTTCTTAGAATTTCTGATGAA 1055
Db 1309 AGCAAAATTTGAAGCTCAGACCAAGGTTAAATCCCTTTCTTAGAATTTCTGATGAA 1368
Qy 1056 TTTATATGTCGAATTAATAGAGAACTTATGAAAGATCCGGTCAATGAGATGAGGCTAT 1115
Db 1369 TTTATATGTCGAATTAATAGAGAACTTATGAAAGATCCGGTCAATGAGATGAGGCTAT 1428
Qy 1116 TCATATGAAAAAGAAAGCAATGAAAAATTGATCAGCAAAAAAGAAACCTACAGTCCCATG 1175
Db 1429 TCATATGAAAAAGAAAGCAATGAAAAATTGATCAGCAAAAAAGAAACCTACAGTCCCATG 1488
Qy 1176 ACAAAATCTTGTCTTCTCTTCAAGCGGTACTTACACCAAAATAGAGATCTGAAAAATGGCCATC 1235
Db 1489 ACAAAATCTTGTCTTCTCTTCAAGCGGTACTTACACCAAAATAGAGATCTGAAAAATGGCCATC 1548
Qy 1236 AATAGATGCTGAGACACACCAAAAGTAAA 1266
Db 1549 AATAGATGCTGAGACACACCAAAAGTAAA 1579

RESULT 5
US-10-956-157-5128
; Sequence 5128, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5128
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5128
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Query Match 75.8%; Score 964.2; DB 22; Length 1821;
Best Local Similarity 81.8%; Pred. No. 2,7e-270;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

Qy 12 TCACCTGCGGAGCAGTGACCCGACCCGCTGGGACCTTGAAGCGGATCCCGCG 71
Db 60 TCACCTGCGGAGCAGTGACCCGACCCGCTGGGACCTTGAAGCGGATCCCGCG 119
Qy 72 CCCCCGCTCTGAGAGCTGTTTTTTCTTCAATTAAGAACTGTGAAACATGATTCACA 131
Db 120 CCCCCGCTCTGAGAGCTGTTTTTTCTTCAATTAAGAACTGTGAAACATGATTCACA 179
Qy 132 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
Db 180 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 239
Qy 192 TGCCTCTTGAGCAAAACAAATGCGCTGATGATGATGATGATGATGATGATGATGAT 251
Db 240 TGCCTCTTGAGCAAAACAAATGCGCTGATGATGATGATGATGATGATGATGATGAT 299
Qy 252 TCTCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
Db 300 TCTCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
Qy 312 ATTTTGGCATGCTGTTCAACAGATGATGATGATGATGATGATGATGATGATGATGAT 371
Db 360 ATTTTGGCATGCTGTTCAACAGATGATGATGATGATGATGATGATGATGATGATGAT 419
Qy 372 ATGCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
Db 420 ATGCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
Qy 432 GACTCCACGCTGTTGGCATGAGGGGACGCTGATGATGATGATGATGATGATGATGAT 491
Db 480 GACTCCACGCTGTTGGCATGAGGGGACGCTGATGATGATGATGATGATGATGATGAT 539
Qy 492 TCATACAAATTAATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
Db 540 TCATACAAATTAATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599
Qy 552 TCTCTTAATGAAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
Db 600 TCTCTTAATGAAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
Qy 612 GATTAATAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
Db 660 GATTAATAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
Qy 672 TTTTCTTCAAGCAGATTTCTGATGAGAAACAAGTCTTCAAGTCTTCAAGTCTTCAAG 731
Db 720 TTTTCTTCAAGCAGATTTCTGATGAGAAACAAGTCTTCAAGTCTTCAAGTCTTCAAG 779
Qy 732 TGTGTCAGAGATTTGCCAAGTCAAAATTTGATGATGATGATGATGATGATGATGATGAT 784
Db 780 TGTGTCAGAGATTTGCCAAGTCAAAATTTGATGATGATGATGATGATGATGATGATGAT 839
Qy 785 ----- 784
Db 840 GAAATTAATAATAAGTACAGTGAAGGACCTGCTCTCTGCTTGCTTGCTTTT 899
Qy 785 ----- 784
Db 900 TCCCATGATGGGAGATGCTAGTCTCAGGCTCAGTGATAGTCTGTCATATATATGAT 959
Qy 785 ----- 784
Db 960 ACTAATACTGAGAAATATACTTCAACATGATGATGATGATGATGATGATGATGATGAT 1019
Qy 785 ----- 784
Db 1020 GCTTTGACCTAATAACCTTTTACTTGCTGATGCTTCAATGACAAAGACATGACATC 1079
Qy 785 ----- -AGCAAGGCGCACAGAACATCAGCTGAACCAA 815
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Db 1080 TGGCAATTTGACCTGGAAACATTGGCCAGCAAGGGGCAAGAACTTCAGCTGAAGCA 1139
QY 816 TTTTACCGAAGATTGGTCAGAGAGGTCGTCTCAACATGGCTTTGTGCAAGATTTTAAA 875
Db 1140 TTTTACCGAAGATTGGTCAGAGAGGTCGTCTCAACATGGCTTTGTGCAAGATTTTAAA 1199
QY 876 GATCTTGTGGTATTTTCAAGATGAATACATGATGATGAAAGAACTGTGAATCTTACA 935
Db 1200 GATCTTGTGGTATTTTCAAGATGAATACATGATGATGAAAGAACTGTGAATCTTACA 1259
QY 936 AAGAAAGTCTGCTGATGATTTGAAAATTGAAATCTCTAGACCTGCGTACGTAAGTCTG 995
Db 1260 AAGAAAGTCTGCTGATGATTTGAAAATTGAAATCTCTAGACCTGCGTACGTAAGTCTG 1319
QY 996 AAGAAATTTGAAGAGCTCAGAGCAAGCAAGTTAAATCCCTTTCTTCAGAAATTCCTGATGA 1055
Db 1320 AAGAAATTTGAAGAGCTCAGAGCAAGCAAGTTAAATCCCTTTCTTCAGAAATTCCTGATGA 1379
QY 1056 TTTATATGTCCTAATTAAGTGAAGATCCGGTCAATGCGATCAGATGAGCTAT 1115
Db 1380 TTTATATGTCCTAATTAAGTGAAGATCCGGTCAATGCGATCAGATGAGCTAT 1439
QY 1116 TCATATGAAAAGAGCAATGAAAATTGGATCAGCAAAAAGAAACGTACAGTCCCATG 1175
Db 1440 TCATATGAAAAGAGCAATGAAAATTGGATCAGCAAAAAGAAACGTACAGTCCCATG 1499
QY 1176 ACAATCTGTTCTTCTCTTCTGAGGGTACTTACACCAATAGACTCTCGAAAATGGCCATC 1235
Db 1500 ACAATCTGTTCTTCTCTTCTGAGGGTACTTACACCAATAGACTCTCGAAAATGGCCATC 1559
QY 1236 AATAGATGCTGGAGACACACCAAAAGTAAA 1266
Db 1560 AATAGATGCTGGAGACACACCAAAAGTAAA 1590

RESULT 6

US-10-037-270-768

; Sequence 768, Application US/10037270

; Publication No. US20030104529A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feijian

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yungqing

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhimei

; APPLICANT: Tillingshaet, John

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/10/037,270

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: 09/552,117

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; NUMBER OF SEQ ID NOS: 1104

; SOFTWARE: pc_Fl_genes Version 1.0

; SEQ ID NO 768

; LENGTH: 1844

; TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-037-270-768

Query Match

75.8%; Score 964.2; DB 16; Length 1844;

Best Local Similarity 81.8%; Prod. No. 2.7e-270;

Matches 1252; Conservative 0; Mismatchen 3; Indels 276; Gaps 1;

QY 12 TCACCTGCGCGGACAGTGCACCGCACCCCGTGGGACCTTGAGGGGATCCCGCGG 71
Db 65 TCACCTGCGCGGACAGTGCACCGCACCCCGTGGGACCTTGAGGGGATCCCGCGG 124
QY 72 CCCCCTCTCTGACAGCTGTTTTCTTCAAAATTAAGAACATGATGAACTGATTCACACA 131
Db 125 CCCCCTCTCTGACAGCTGTTTTCTTCAAAATTAAGAACATGATGAACTGATTCACACA 184
QY 132 TTAGCTGATCATGATGACGATGCACTGCTGCTTCTCTTTTCCCTTTGCTACT 191
Db 185 TTAGCTGATCATGATGACGATGCACTGCTGCTTCTCTTTTCCCTTTGCTACT 244
QY 192 TGCTCTTGGAACAAACATTTGGCTGTACTGTTACGTGACTTTACGATGCGACAT 251
Db 245 TGCTCTTGGAACAAACATTTGGCTGTACTGTTACGTGACTTTACGATGCGACAT 304
QY 252 TCTCCATTGAAGTTTCAATACCTAATGCTGTCACATGCTGCTGTTTCCCTTCAGACAT 311
Db 305 TCTCCATTGAAGTTTCAATACCTAATGCTGTCACATGCTGCTGTTTCCCTTCAGACAT 364
QY 312 ATTTTGGCATCGTGTTCACACAGATGGTACCACTGTCCTATGGAATACGAAAATGACAG 371
Db 365 ATTTTGGCATCGTGTTCACACAGATGGTACCACTGTCCTATGGAATACGAAAATGACAG 424
QY 372 ATGCTGCACTGATGGAACAGCTAATGAGCAGCCCTGTAGAGGTTTGGCAATTTCCCA 431
Db 425 ATGCTGCACTGATGGAACAGCTAATGAGCAGCCCTGTAGAGGTTTGGCAATTTCCCA 484
QY 432 GACTCCAGCTGTTTGGCATCAGGGGACGTGAATGAACTGTGTTTGTGAAATGACAG 491
Db 485 GACTCCAGCTGTTTGGCATCAGGGGACGTGAATGAACTGTGTTTGTGAAATGACAG 544
QY 492 TCATCAAAATTAAT 551
Db 545 TCATCAAAATTAAT 604
QY 552 TCTCCTTAATGAACTTCTTTTGTCACTGGCTCTCTCATGTGTGATTTAACAGTGGGAT 611
Db 605 TCTCCTTAATGAACTTCTTTTGTCACTGGCTCTCTCATGTGTGATTTAACAGTGGGAT 664
QY 612 GATAAATAGAGTGTCTGATAGTGAAGAACATGATCTTGAAATTAAGTCTGAT 671
Db 665 GATAAATAGAGTGTCTGATAGTGAAGAACATGATCTTGAAATTAAGTCTGAT 724
QY 672 TTTTCTTCAACAGCAAGCTTTCTGATGGAACAGAGTCTTCAAGTTTTCGACTGGCATCA 731
Db 725 TTTTCTTCAACAGCAAGCTTTCTGATGGAACAGAGTCTTCAAGTTTTCGACTGGCATCA 784
QY 732 TGTGTGACAGATTTGCCAAGTCAAAATTTGATTTGTTCTTTAACCAATCTT----- 784
Db 785 TGTGTGACAGATTTGCCAAGTCAAAATTTGATTTGTTCTTTAACCAATCTT----- 844
QY 785 ----- 784
Db 845 GAATTAATAATTAAGTACACAGATGGGCACTGTGCTCTGTTCTGGCTGTGCTTTT 904
QY 785 ----- 784
Db 905 TCCCATGATGGGACAGATGCTAGTCTCAGGGTCAATGATGATGATGATGATGATGATGAT 964
QY 785 ----- 784
Db 965 ACTAATACTGAGAAATTAATCTTCAACATTTGACTCAGCACACCAAGTATGTCAACACTTGT 1024


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QY 785 ----- 784
Db 1025 GCTTTGCACTAATACCCCTTTACTGTCTACTGTTCATGACAAACAGTAAATC 1084
QY 785 -----AGCAAGCGCACAGAACATCAGCTGAACAA 815
Db 1085 TGGCAATTTGACCTGAAACCTTTGCCAAGCAAGACAGAACATCAGCTGAACAA 1144
QY 816 TTTTACGAAATGCTAGAGAGAGGTGTCTCAACATGCGCTTGTGCAAGATTTTAAA 875
Db 1145 TTTTACGAAATGCTAGAGAGAGGTGTCTCAACATGCGCTTGTGCAAGATTTTAAA 1204
QY 876 GATCTGTGTGTAATTTTCAAGATGAATACCTGATGAAAGAACTGTTGAATCTTACA 935
Db 1205 GATCTGTGTGTAATTTTCAAGATGAATACCTGATGAAAGAACTGTTGAATCTTACA 1264
QY 936 AAAGAAAGTCTGCTGATGATTTGAAATCTCTAGAGCTGCGTGAATAGTCTG 995
Db 1265 AAAGAAAGTCTGCTGATGATTTGAAATCTCTAGAGCTGCGTGAATAGTCTG 1324
QY 996 AGCAAAATTTGAAGCTCAGAGACCAAGTTAAATCCCTTTCTTGAAGATTTCTGATGAA 1055
Db 1325 AGCAAAATTTGAAGCTCAGAGACCAAGTTAAATCCCTTTCTTGAAGATTTCTGATGAA 1384
QY 1056 TTTTATGTCCAAATTAATAGAACTTATGAAAGATCGGTCATCGCATCAGATGCGTAT 1115
Db 1385 TTTTATGTCCAAATTAATAGAACTTATGAAAGATCGGTCATCGCATCAGATGCGTAT 1444
QY 1116 TCATATGAAAAAGAGCAATGGAATTTGATCAGCAAAAAAGAAACGTACAGTCCCATG 1175
Db 1445 TCATATGAAAAAGAGCAATGGAATTTGATCAGCAAAAAAGAAACGTACAGTCCCATG 1504
QY 1176 ACAAAATTTGTTCTTCTTCAAGCGGTACTTAACCAAAATAGAACTCGAAAAATGGCATC 1235
Db 1505 ACAAAATTTGTTCTTCTTCAAGCGGTACTTAACCAAAATAGAACTCGAAAAATGGCATC 1564
QY 1236 AATAGATGCTGAGACACACCAAAAGTAAA 1266
Db 1565 AATAGATGCTGAGACACACCAAAAGTAAA 1595

RESULT 7
US-10-117-722-768
; Sequence 768, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 768
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-117-722-768
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Query Match 75.8%; Score 964.2; DB 18; Length 1844;
Best Local Similarity 81.8%; Pred. No. 2,7e-270;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY 12 TCACCTGCGGGACGCTGACCCGCCACCGCGTGGGCACTTGAAGCGGATCCCGCG 71
Db 65 TCACCTGCGGGACGCTGACCCGCCACCGCGTGGGCACTTGAAGCGGATCCCGCG 124
QY 72 CCCCCGCTCTGACAGGTGTTTTTCTTCAATTAAGAACTGTGAACTGATTCACACA 131
Db 125 CCCCCGCTCTGACAGGTGTTTTTCTTCAATTAAGAACTGTGAACTGATTCACACA 184
QY 132 TTAGCTGATCATGTGACGATGTCACACTGCTGACCTTCCCTTTCCCTTGGCTACT 191
Db 185 TTAGCTGATCATGTGACGATGTCACACTGCTGACCTTCCCTTTCCCTTGGCTACT 244
QY 192 TGCTCTTGGACAAACAAATTCCTGTACTGCTTACGTAAGTCTTACGAACTGCCACAT 251
Db 245 TGCTCTTGGACAAACAAATTCCTGTACTGCTTACGTAAGTCTTACGAACTGCCACAT 304
QY 252 TCTCCATTTGAAGTTTCTTACCTATGCTGTCACTGCTGCTGTTTCCCTTCAAGCAT 311
Db 305 TCTCCATTTGAAGTTTCTTACCTATGCTGTCACTGCTGCTGTTTCCCTTCAAGCAT 364
QY 312 ATTTTGGCATCGTGTTCACAGATGGTACCACTGCTCCTATGAAATACTGAAATGACAG 371
Db 365 ATTTTGGCATCGTGTTCACAGATGGTACCACTGCTCCTATGAAATACTGAAATGACAG 424
QY 372 ATGCTGCACTGATGGAACAGCTTACGTAGGAGCCCTGTGAGGCTTGGCAGTTTCCCA 431
Db 425 ATGCTGCACTGATGGAACAGCTTACGTAGGAGCCCTGTGAGGCTTGGCAGTTTCCCA 484
QY 432 GACTCCACGTTTGGCATATAGGGGACGCTGATGGAACCTGCTGTTTGGAAATGACAG 491
Db 485 GACTCCACGTTTGGCATATAGGGGACGCTGATGGAACCTGCTGTTTGGAAATGACAG 544
QY 492 TCATACAAATTAATATAGATGTGTAGTGTAAAGATGCTCTTGGCGCATGTCATTT 551
Db 545 TCATACAAATTAATATAGATGTGTAGTGTAAAGATGCTCTTGGCGCATGTCATTT 604
QY 552 TCTCCTAATGAAAGCTTCTTGTCACTGCTCTCATGTGTGATTTAACAGTGGGAT 611
Db 605 TCTCCTAATGAAAGCTTCTTGTCACTGCTCTCATGTGTGATTTAACAGTGGGAT 664
QY 612 GATPAAATGAGGTGTCTGCAATAGTAAAGACATGATCTTGGAAATTACTCTGCGAT 671
Db 665 GATPAAATGAGGTGTCTGCAATAGTAAAGACATGATCTTGGAAATTACTCTGCGAT 724
QY 672 TTTTCTTCAAGCCAGTTTCTGATGGAACCAAGTCTTCAATTTTTCGACTGGCATCA 731
Db 725 TTTTCTTCAAGCCAGTTTCTGATGGAACCAAGTCTTCAATTTTTCGACTGGCATCA 784
QY 732 TGTGTCAGGATTTGCCAAGTCAAAATTTGGATGTTTCTTTTAAACCATATCTT----- 784
Db 785 TGTGTCAGGATTTGCCAAGTCAAAATTTGGATGTTTCTTTTAAACCATATCTT----- 844
QY 785 ----- 784
Db 845 GAAATTAATATAAAGTACACTGATGGGCACTGTGCTCTGCTTCTGCTGTGCTTTT 904
QY 785 ----- 784
Db 905 TCCCATGATGGGAGATGCTAGTCTCAGGCTCAGTGAATAGTCTGTCATAGTATATGAT 964
QY 785 ----- 784
Db 965 ACTAATACAGATAATACTTCAACATGACTCAGACACACAGTATGTCACAATTTGT 1024
QY 785 ----- 784
Db 1025 GCTTTTGCACCTAATACCTTTTACTTGTCTACTGTTCATATGACAAACAGTAAATC 1084
QY 785 -----AGCAAGCGCACAGAACATCAGCTGAACAA 815
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Db 1085 TGGCAATTTGACCTGGAAACCTTGGCCAAGAGGACACAAATCATCGTGAAGCAA 1144
QY 816 TTTTACGGAAGATTGGTCAGAGGAGTGTCTCAACATGCTTTGTGCAACAAGTTTAAAA 875
Db 1145 TTTTACGGAAGATTGGTCAGAGGAGTGTCTCAACATGCTTTGTGCAACAAGTTTAAAA 1204
QY 876 GATCTGTGTGATTTTTCAGATGATTAACATGATGAGAAAAGAACTGTGAATCTTACA 935
Db 1205 GATCTGTGTGATTTTTCAGATGATTAACATGATGAGAAAAGAACTGTGAATCTTACA 1264
QY 936 AAGAAAGTCTGGCTGATGATTTGAAAATTTCTTGAAGTGGCTAGTAAAGTCTG 995
Db 1265 AAGAAAGTCTGGCTGATGATTTGAAAATTTCTTGAAGTGGCTAGTAAAGTCTG 1324
QY 996 AAGAAATTTGAAGAGCTCAGAGCAACCAAGTTAAATCCCTTTCTTCAAGAAATCTGATGAA 1055
Db 1325 AAGAAATTTGAAGAGCTCAGAGCAACCAAGTTAAATCCCTTTCTTCAAGAAATCTGATGAA 1384
QY 1056 TTTATATGTCATTAATAGAGAACTTATGAAGATCCGCTCATCGCATGAGTGGCTAT 1115
Db 1385 TTTATATGTCATTAATAGAGAACTTATGAAGATCCGCTCATCGCATGAGTGGCTAT 1444
QY 1116 TCATATGAAAAAGAGCAATGAAAAATTTGATCAGCAAAAAAGAAAGCTACAGTCCCATG 1175
Db 1445 TCATATGAAAAAGAGCAATGAAAAATTTGATCAGCAAAAAAGAAAGCTACAGTCCCATG 1504
QY 1176 ACAAAATCTTGTCTTCTTCTTACGGCTACTTACACCAAAATGAGCTCGAAAAATGGCATC 1235
Db 1505 ACAAAATCTTGTCTTCTTCTTACGGCTACTTACACCAAAATGAGCTCGAAAAATGGCATC 1564
QY 1236 AATAGATGGCTGGAGACACACCAAAAAGTAAA 1266
Db 1565 AATAGATGGCTGGAGACACACCAAAAAGTAAA 1595

RESULT 8

US-10-287-218-40
; Sequence 40; Application US/10287218
; Publication No. US20030198975A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.
; APPLICANT: BATRA, Sajeev; BAUGHN, Mariah R.
; APPLICANT: BECHA, Shanya D.; BOROMSKY, Mark L.
; APPLICANT: BUFOED, Neil; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
; APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: HONCHELL, Cynthia D.; LAU, Preeti G.
; APPLICANT: LEE, Soo Yeun; LU, Dying; Alina M.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: REDDY, Roopa; SANDANMALA, Madhu, M.
; APPLICANT: TANG, Y. Tom; WALIA, Nalinder K.
; APPLICANT: WANG, Yu-mei, E.; WARREN, Bridget A.
; APPLICANT: XU, Yuming; YANG, Junming
; APPLICANT: YAO, Monique G.; YUE, Henry
; APPLICANT: ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: P1-0417 USA
; CURRENT APPLICATION NUMBER: US/10/287,218
; PRIOR APPLICATION NUMBER: PCT/US02/11152
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/11152
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/349,705
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/295,263
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/295,340
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/293,727
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/291,846

; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/291,662
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/287,228
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/286,820
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/283,294
; PRIOR FILING DATE: 2001-04-11
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030198975A1 7403131CB1
US-10-287-218-40

Query Match 70.3%; Score 894; DB 17; Length 1773;
Best Local Similarity 80.6%; Pred. No. 8,6e-250;
Matches 1186; Conservative 0; Mismatches 10; Indels 276; Gaps 1;

QY 71 GCCCGCGCTCCGACGCTGTTTCTTCAATTAAGAAATGTAAGTATGATTCACAC 130
Db 20 GCGGCGGTGCGGCGAGCGTGTCTTCTTCAATTAAGAAATGTAAGTATGATTCACAC 79
QY 131 ATTAGCTGATCATGTGAGATGATCAACTGTGTGCTTCTCTTTCCCTTGGCTAC 190
Db 80 ATTAGCTGATCATGTGAGATGATCAACTGTGTGCTTCTCTTTCCCTTGGCTAC 139
QY 191 TTGCTCTTGGACAAACAAATTCGCTGTACTGCTTAACTGATGAACTGCAACA 250
Db 140 TTGCTCTTGGACAAACAAATTCGCTGTACTGCTTAACTGATGAACTGCAACA 199
QY 251 TTCTCATTAAGATTTTCAATACCTATGCTGTGCTGCTGCTGCTTTCCTCCCTTCAAGACA 310
Db 200 TTCTCATTAAGATTTTCAATACCTATGCTGTGCTGCTGCTGCTTTCCTCCCTTCAAGACA 259
QY 311 TATTTTGGATCGTGTTCACACAGATGTAACAATGCTGCTTATGAAATATGAAATGGACA 370
Db 260 TATTTTGGATCGTGTTCACACAGATGTAACAATGCTGCTTATGAAATATGAAATGGACA 319
QY 371 GATGCTGGAGATGATGAAACAGCTTATGTCAGACCTGTGAGAGGTTTGGCAATTTCCCC 430
Db 320 GATGCTGGAGATGATGAAACAGCTTATGTCAGACCTGTGAGAGGTTTGGCAATTTCCCC 379
QY 431 AGACTCCAGCTGTTTGGCATCAGGGGACAGCTGATGGAACATGTTTGTGAAATGACA 490
Db 380 AGACTCCAGCTGTTTGGCATCAGGGGACAGCTGATGGAACATGTTTGTGAAATGACA 439
QY 491 GTCATACAAATATATATAGATGTGTATGATGTAAGATGCTCTTGGCGGATGTGCATT 550
Db 440 GTCATACAAATATATATAGATGTGTATGATGTAAGATGCTCTTGGCGGATGTGCATT 499
QY 551 TTCTCTTAATGAAAGCTTCTTGTGCTACTGCTGCTTATGATGATTTTAAAGTGTGGA 610
Db 500 TTCTCTTAATGAAAGCTTCTTGTGCTACTGCTGCTTATGATGATTTTAAAGTGTGGA 559
QY 611 TGAATAAATGAGGTGCTGATAGTAAAGAAACATGATCTTGGAAATTAACGCTGCGCA 670
Db 560 TGAATAAATGAGGTGCTGATAGTAAAGAAACATGATCTTGGAAATTAACGCTGCGCA 619
QY 671 TTTTCTTCAAGCCAGTTTGTGATGAGAAACAGAGTCTTCAAGTTTTCGACTGGCATC 730
Db 620 TTTTCTTCAAGCCAGTTTGTGATGAGAAACAGAGTCTTCAAGTTTTCGACTGGCATC 679
QY 731 ATGTGTCAGATTTGCAAGTCAAAATTTGATTTGTTCTTTTAAACCATATCTT----- 784
Db 680 ATGTGTCAGATTTGCAAGTCAAAATTTGATTTGTTCTTTTAAACCATATCTTAAAGTTT 739

QY	785	-----	784
Db	740	TGAATTAATAATATAAAAGTACACTGAGTGGGACCTGCTCTTCTGCTTGGCTTGCTTT	799
QY	785	-----	784
Db	800	TTCCCATGATGGGAGATGCTAGTCTCAGGGGTCAGTGGATAAAGTCTGATCATAGTATATGA	859
QY	785	-----	784
Db	860	TACTAATACTGAGAATATATCTTCAACATTTGACTCAGCACACGAGATATGTCACAACTTG	919
QY	785	-----	784
Db	920	TGCTTTTGACCTTAATACCTTTTACTTGCTACTGTTGTAATGACAAACAGTGAAACAT	979
QY	785	-----AGCAAGGCGCACAGAACTCAGCTGAAGCA	814
Db	980	CTGGCAATTTTGACCTGGAAACACTTTTGCCAGCACAGGAGGCAACAGATCTGAGTGAAGCA	1039
QY	815	ATTATACGAGAGATTGGTCTCAGAGAGGTGCTCAACATGGCTTTGTGCACAAGATTTTAA	874
Db	1040	ATTATACGGAATTTGGTCTCAGAGAGAGATGCTCAACAATGCTCTTGTGCACAAGATTTTAA	1099
QY	875	AGATCTTGGTGATTTTTCAGAGATGAATAATGATGAGAAAGAACTGTGGAATCTTAC	934
Db	1100	AGATCTTGGTGATTTTTCAGAGATGAATAATGATGAGAAAGAACTGTGGAATCTTAC	1159
QY	935	AAAGAAAGTGTGGCTGATGATTTTGAATAATTGAATCTTAGAGCTGGCGTAGTAAAGTCT	994
Db	1160	AAAGAAAGTGTGGCTGATGATTTTGAATAATTGAATCTTAGAGCTGGCGTAGTAAAGTCT	1219
QY	995	GAGAAAAATTGSAAGCTCAGAGCCAAAGTTAAATCCCTTTCTTCAGGAATTCCTGATGA	1054
Db	1220	GAGAAAAATTGSAAGCTCAGAGCCAAAGTTAAATCCCTTTCTTCAGGAATTCCTGATGA	1279
QY	1055	ATTATATATGTCCTCAATACTAGAGAACTTATGAAAGATTCGGTCACTGGCATAGATGGCTA	1114
Db	1280	ATTATATATGTCCTCAATACTAGAGAACTTATGAAAGATTCGGTCACTGGCATAGATGGCTA	1339
QY	1115	TTCAATATGAAAGGAAAGCAATGAGAAATTTGATGAGCAAAAAGAAAGCTACAGTCCCAT	1174
Db	1340	TTCAATATGAAAGGAAAGCAATGAGAAATTTGATGAGCAAAAAGAAAGCTACAGTCCCAT	1399
QY	1175	GACAAATCTTGTCTTCTCTTCAGCGGTACTTACCAAAATGAGACTGTGAAAATGGCCAT	1234
Db	1400	GACAAATCTTGTCTTCTCTTCAGCGGTACTTACCAAAATGAGACTGTGAAAATGGCCAT	1459
QY	1235	CAATAGATGGCTGGAGACACACCAAAAGTTAA	1266
Db	1460	CAATAGATGGCTGGAGACACACCAAAAGTTAA	1491
RESULT 9			
US-10-474-291-40			
; Sequence 40, Application US/10474291			
; Publication No. US20040132043A1			
; GENERAL INFORMATION:			
; APPLICANT: AZIMZAI, Valda; AU-YOUNG, Janice K.			
; APPLICANT: BATRA, Sajeev; BAUGHN, Mariah R.			
; APPLICANT: BECHA, Shanya D.; BOROWSKI, Mark L.			
; APPLICANT: BURFORD, Neil; DING, Li			
; APPLICANT: ELIOTT, Vicki S.; EMERLING, Brooke M.			
; APPLICANT: GANDHI, Ameena R.; GIERZEN, Kimberly J.			
; APPLICANT: GRIFFIN, Jennifer A.; HAPFLA, April J.A.			
; APPLICANT: HONCHELL, Cynthia D.; IAL, Preeti G.			
; APPLICANT: LEE, Soo Yeun; LU, Dying Anna M.			
; APPLICANT: ARVIZU, Chandra S.; RANKUMAR, Jayalaxmi			
; APPLICANT: REDDY, Roopa M.; SANJAYAWALA, Madhusudan M.			
; APPLICANT: TANG, Y. Tom; CHAWLA, Narinder K.			
; APPLICANT: WANG, Yu-Mei E.; WARREN, Bridget A.			
; APPLICANT: XU, Yuning; YANG, Junning			
; APPLICANT: YAO, Monique G.; YUE, Henry			

```

1  TITLE OF INVENTION: ZEBRAFADIAN, Yeganeh
2  FILE REFERENCE: PI-0417 USN
3  CURRENT APPLICATION NUMBER: US/10/474, 291
4  CURRENT FILING DATE: 2003-10-06
5  PRIOR APPLICATION NUMBER: PCT/US02/11152
6  PRIOR FILING DATE: 2002-04-05
7  PRIOR APPLICATION NUMBER: US 60/349, 705
8  PRIOR FILING DATE: 2002-01-15
9  PRIOR APPLICATION NUMBER: US 60/295, 263
10 PRIOR FILING DATE: 2001-06-01
11 PRIOR APPLICATION NUMBER: US 60/295, 340
12 PRIOR FILING DATE: 2001-06-01
13 PRIOR APPLICATION NUMBER: US 60/293, 727
14 PRIOR FILING DATE: 2001-05-25
15 PRIOR APPLICATION NUMBER: US 60/291, 846
16 PRIOR FILING DATE: 2001-05-18
17 PRIOR APPLICATION NUMBER: US 60/291, 662
18 PRIOR FILING DATE: 2001-05-16
19 PRIOR APPLICATION NUMBER: US 60/287, 228
20 PRIOR FILING DATE: 2001-04-27
21 PRIOR APPLICATION NUMBER: US 60/286, 820
22 PRIOR FILING DATE: 2001-04-26
23 PRIOR APPLICATION NUMBER: US 60/283, 294
24 PRIOR FILING DATE: 2001-04-11
25 Remaining Prior Application data removed - See File Wrapper or PMLM.
26 NUMBER OF SEQ ID NOS: 42
27 SOFTWARE: PERL Program
28 SEQ ID NO 40
29 LENGTH: 1773
30 TYPE: DNA
31 ORGANISM: Homo sapiens
32 FEATURE:
33 NAME/KEY: misc_feature
34 OTHER INFORMATION: Incyte ID No: 7483131CBI
35 US-10-474-291-40

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Query Match	70.3%	Score 894	DB 20	Length 1773
Best Local Similarity	80.6%	Pred. No. 8.6e-250		
Matches 1186	Conservative 0	Mismatches 10	Indels 276	Gaps 1
QY	71	GCCTCCGCTCTCGAGCGCTGTTTTCTTCAAAATAAGAAACATGTGAACATGATTCACAC	130	
Db	20	GCCTCCGCTCTCGAGCGCTGTTTTCTTCAAAATAAGAAACATGTGAACATGATTCACAC	79	
QY	131	ATTGACGTATCATGGTGACGATGTCACATGCTGTGACCTTCACTTTCCTCTTGCGTAC	190	
Db	80	ATTGACGTATCATGGTGACGATGTCACATGCTGTGACCTTCACTTTCCTCTTGCGTAC	139	
QY	191	TTGCTCTCTTGACAAAACAAATTGCGCTGACTGCTGTACGTGATCTTTACTGAACATGCCACA	250	
Db	140	TTGCTCTCTTGACAAAACAAATTGCGCTGACTGCTGTACGTGATCTTTACTGAACATGCCACA	199	
QY	251	TTTCCTCATTAAGTTTTATATACCTATGCTGTGTCACATGCTGCTGTTTCTCCCTTGAGACA	310	
Db	200	TTTCCTCATTAAGTTTTATATACCTATGCTGTGTCACATGCTGCTGTTTCTCCCTTGAGACA	259	
QY	311	TATTTTGGCATCGTGTTCMAACAGATGTGATCACATGTCCTATGAGATATCTGAATAATGACA	370	
Db	260	TATTTTGGCATCGTGTTCMAACAGATGTGATCACATGTCCTATGAGATATCTGAATAATGACA	319	
QY	371	GATGCTGGCATGATNGAACAGCCTAGTGGGAGCCCTGTAGAGGTTTGGCAGTTTTTCCC	430	
Db	320	GATGCTGGCATGATNGAACAGCCTAGTGGGAGCCCTGTAGAGGTTTGGCAGTTTTTCCC	379	
QY	431	AGACTCCACGCTGTTTGGCATCAGGGGCGACGTATGAGAACTGTGTTTTGTGGAATGACA	490	
Db	380	AGACTCCACGCTGTTTGGCATCAGGGGCGACGTATGAGAACTGTGTTTTGTGGAATGACA	439	
QY	491	GTCATTAACAAATTATATATGATGTGGTAGTGTGTTAAAGATGGCTCTTGGCGGACATGTGCATT	550	
Db	440	GTCATTAACAAATTATATATGATGTGGTAGTGTGTTAAAGATGGCTCTTGGCGGACATGTGCATT	499	

QY 551 TTCTCTAATGAGAGCTTTCTTGTCACTGCTCCTCATGHTGTGATTTAACTAGTGGGA 610
| | | | |
Db 500 TTCTCTAATGAGAGCTTTCTTGTCACTGCTCCTCATGHTGTGATTTAACTAGTGGGA 559
| | | | |
QY 611 TGATAAAATGAGGTGTCTGCATAGTGAAGAAAAGACATGATCTTGAATTAACCTGCTGGCA 670
| | | | |
Db 560 TGATAAAATGAGGTGTCTGCATAGTGAAGAAAAGACATGATCTTGAATTAACCTGCTGGCA 619
| | | | |
QY 671 TTTTCTTCAACGCCAGTTCTGTATGAGAGAACAAAGCTTCAATTTTGTGATCTGGCATC 730
| | | | |
Db 620 TTTTCTTCAACGCCAGTTCTGTATGAGAGAACAAAGCTTCAATTTTGTGATCTGGCATC 679
| | | | |
QY 731 ATGTGCTCAGAGTTGCTCAAGTCAAAAATTTGATTTGTTCTTTTACCATACTT----- 784
| | | | |
Db 680 ATGTGCTCAGAGTTGCTCAAGTCAAAAATTTGATTTGTTCTTTTACCATACTTAGGTTT 739
| | | | |
QY 785 ----- 784
| | | | |
Db 740 TGAATTAATAATATAAAAGTACACTGAGTGGGCACTGTGCTCTGTCTGTGCTTGTGCTTT 799
| | | | |
QY 785 ----- 784
| | | | |
Db 800 TTCCCATGATGGCAGATGCTAGTCTCAGGGTCAAGTGAATAGTCTGTCAATGATATGA 859
| | | | |
QY 785 ----- 784
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Db 860 TACTAATACTGAGATATATCTTCAACATTTGACTCAGACACACAGGATATGCAAACTTG 919
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QY 785 ----- 784
| | | | |
Db 920 TGTCTTTGACCTTAATACCTTTTACTTGTCTACTGTGTTCAATGAGCAAAAACAGTGAACAT 979
| | | | |
QY 785 ----- 814
| | | | |
Db 980 CTGGCAATTTGACCTGAGAAACACTTTGCCAAGCAGAGAGCAAGAACATATAGCTGAAGCA 1039
| | | | |
QY 815 ATTTACCGAAGATTGCTCAGAGAGAGTCTGTCTCAACATGCTTTGTGCACAAAGATTTAA 874
| | | | |
Db 1040 ATTTACCGAAGATTGCTCAGAGAGAGTGTCTCAACATGCTTTGTGCACAAAGATTTAA 1099
| | | | |
QY 875 AGATCTTTGTTGGTATTTTCAAGATGAATTAACATTGATGAAAAAGAACTGTTGAATCTTAC 934
| | | | |
Db 1100 AGATCTTTGTTGGTATTTTCAAGATGAATTAACATTGATGAAAAAGAACTGTTGAATCTTAC 1159
| | | | |
QY 935 AAAAAGAAAGTCTGATGATTTGAAAAATGAAATCTTAGACACTGGCTAGTAAAGTCT 994
| | | | |
Db 1160 AAAAAGAAAGTCTGATGATTTGAAAAATGAAATCTTAGACACTGGCTAGTAAAGTCT 1219
| | | | |
QY 995 GAGAAAAATTGAAGCTCAGACCAAGGTTAAATCCCTTTCTTCAAGAAATCTCTGATGA 1054
| | | | |
Db 1220 GAGAAAAATTGAAGCTCAGACCAAGGTTAAATCCCTTTCTTCAAGAAATCTCTGATGA 1279
| | | | |
QY 1055 ATTTAATATGCTCAATACTAGAGACTTATGAAAAAGATCCGGTCACTGCATCAATGGCTTA 1114
| | | | |
Db 1280 ATTTAATATGCTCAATACTAGAGACTTATGAAAAAGATCCGGTCACTGCATCAATGGCTTA 1339
| | | | |
QY 1115 TTCTATGAAAAAGAAAGCAATGAAAAATTTGATCAGCAAAAAAGAAAGCTCAAGTCCCAT 1174
| | | | |
Db 1340 TTCTATGAAAAAGAAAGCAATGAAAAATTTGATCAGCAAAAAAGAAAGCTCAAGTCCCAT 1399
| | | | |
QY 1175 GACAAATCTTTGTTCTTCTTCAAGCGGTACTTACACCAAAATAGGACTCTGAAAAATGGCCAT 1234
| | | | |
Db 1400 GACAAATCTTTGTTCTTCTTCAAGCGGTACTTACACCAAAATAGGACTCTGAAAAATGGCCAT 1459
| | | | |
QY 1235 CATATAGTGGCTGAGACACACCAAAAGTAAA 1266
| | | | |
Db 1460 CATATAGTGGCTGAGACACACCAAAAGTAAA 1491
| | | | |

RESULT 10

US-10-104-047-1689
; Sequence 1689, Application US/10104047
; Publication No. US20030236392A1

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1689
; LENGTH: 1811
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1689

Query Match 70.0%; Score 890.2; DB 18; Length 1811;
Best Local Similarity 80.9%; Pred. No. 1.1e-248;
Matches 1178; Conservative 0; Mismatches 33; Indels 276; Gaps 1;

QY 86 GGCTGTTTTCTTCAATAAAGAACATGAGAACTGATTCACACATTAAGCTGATCATG 145
| | | | |
Db 125 GGCTGTTTTCTTCAATAAAGAACATGAGAACTGATTCACACATTAAGCTGATCATG 184
| | | | |
QY 146 TGAAGATGCACTGCTGTGCTCTCTCTTTCCCTTTGGCTACTTGTCTTGACAA 205
| | | | |
Db 185 TGAAGATGCACTGCTGTGCTCTCTCTTTCCCTTTGGCTACTTGTCTTGACAA 244
| | | | |
QY 206 AACAAATTCGCTGTACTCTGTACGTACTTTACTGAACCTGCCAATTCTGCATTGAAGTT 285
| | | | |
Db 245 AACAAATTCGCTGTACTCTGTACGTACTTTACTGAACCTGCCAATTCTGCATTGAAGTT 304
| | | | |
QY 266 TCATACCTATGCTGTCACATGCTGCTGTTTCTCCCTTCAAGGACATATTTGGCATCGTG 325
| | | | |
Db 305 TCATACCTATGCTGTCACATGCTGCTGTTTCTCCCTTCAAGGACATATTTGGCATCGTG 364
| | | | |
QY 326 TTCAACAGATGATACCACTGCTCTATGAAATCTGAAAAATGACAGATCTGGCAGTAT 385
| | | | |
Db 365 TTCAACAGATGATACCACTGCTCTATGAAATCTGAAAAATGACAGATCTGGCAGTAT 424
| | | | |
QY 386 GGAACAGCTAGTGGCAGCCCTGTAGAGTTTGGCCAGTTTCCCGACATCCAGTGTCTT 445
| | | | |
Db 425 GGAACAGCTAGTGGCAGCCCTGTAGAGTTTGGCCAGTTTCCCGACATCCAGTGTCTT 484
| | | | |
QY 446 GGCATAGGGGAGCGCTGATGGAACCTGTGTTTGTGAAATGCAACATCAAAATTATA 505
| | | | |
Db 485 GGCATAGGGGAGCGCTGATGGAACCTGTGTTTGTGAAATGCAACATCAAAATTATA 544
| | | | |
QY 506 TAGATGTGTAGTGTAAAGATGGCTCTTGGCGCATGTGATTTCTCTAATGGAAG 565
| | | | |
Db 545 TAGATGTGTAGTGTAAAGATGGCTCTTGGCGCATGTGATTTCTCTAATGGAAG 604
| | | | |
QY 566 CTTCCTTTGTCATGCTGCTCTCTCATGTGTGATTTAACAAGTGTGGAGATGAATAGGCTG 625
| | | | |
Db 605 CTTCCTTTGTCATGCTGCTCTCTCATGTGTGATTTAACAAGTGTGGAGATGAATAGGCTG 664
| | | | |
QY 626 TCTGCAATGAAAAAGCAATGATCTTGAATTTACTCTGCGATTTTCTTCAACAGCC 685
| | | | |
Db 665 TCTGCAATGAAAAAGCAATGATCTTGAATTTACTCTGCGATTTTCTTCAACAGCC 724
| | | | |
QY 686 AGTTTCTGATGAGAACCAAGGCTTTCAGTTTTCGATGCGCATCATGTGTGATGAGATTG 745
| | | | |
Db 725 AGTTTCTGATGAGAACCAAGGCTTTCAGTTTTCGATGCGCATCATGTGTGATGAGATTG 784
| | | | |
QY 746 CCAAGTCAAAATTTGGATGTTTCTTTTACCATACTT----- 784
| | | | |
Db 785 CCAAGTCAAAATTTGGATGTTTCTTTTACCATACTT----- 844
| | | | |
QY 785 ----- 784
| | | | |
Db 845 AAGTACACTGATGGGCACTGTGCTCTGCTTGTGCTTGTTCATGATGAGGCA 904
| | | | |
QY 785 ----- 784
| | | | |

D	b		965	GATGCTAGTCTCAGGGGTCAGTGGAATAAGTCCTGTCAATGATATGATTACTAATACTGAGAA	964
O	y		785	-----	784
D	b		965	TATACCTCACATTTGACTCAGACAACCAGGTAATGCACAACTTGCTTTTGACCTTAA	1022
O	y		785	-----	784
D	b		1025	TACCCTTTTACTGCTGTAAGTGTCTCAATGAGACAAAACAGTGAACATCTGGCAATTTGACCT	1084
O	y		785	-----AGCAAGCGCACAGAACATCATGCAAGCTGAAGAATTTACCGAAGATTG	829
D	b		1085	GGAACACTTTTGCCACAGCAAGAGACACAGACATCAGCTGAAGCAATTTACCGAAGATTG	1144
O	y		830	GTCAGAGAGGTCGTCTCAACATGCGCTTTGTGACAGAATTTAAAAAGATCTTGTGTGAT	889
D	b		1145	GTCAGAGAGAGATGTCTCAACATGGCTTTGTGACAGAATTTAAAAAGATCTTGTGTGAT	1200
O	y		890	TTTCAAGATGAATTAACATTGATGAGAAAAGACTGTTGAATCTTACAAAAGAAAGTCTGCC	949
D	b		1205	TTTCAAGATGAATTAACATTGATGAGAAAAGACTGTTGAATCTTACAAAAGAAAGTCTGCC	1266
O	y		950	TGATGATTTGAAAAATTGAATCTCTGAGACTGCGTGTGTAAGCGTCGAGAGAAAATTGAAGA	1000
D	b		1265	TGATGATTTGAAAAATTGAATCTCTGAGACTGCGTGTGTAAGCGTCGAGAGAAAATTGAAGA	1322
O	y		1010	GCTCAGAGCAACAAGTTAAATCCCTTCTTCAGAGAATTCCTGATGAATTTATATGTCCAAT	1065
D	b		1325	GCTCAGAGCAACAAGTTAAATCCCTTCTTCAGAGAATTCCTGATGAATTTATATGTCCAAT	1380
O	y		1070	AACCTAGAGAACTTATGAAAAGATCCGCGTCATCGCATCGATGAGCTTATTCATATGAAAAGGA	1122
D	b		1385	AACCTAGAGAACTTATGAAAAGATCCGCGTCATCGCATCGATGAGCTTATTCATATGAAAAGGA	1444
O	y		1130	AGCAATGGAATAATTGGATTCAGAAAAAGAAAGCTCAAGTCCCAGACAAATCTTGTCT	1188
D	b		1445	AGCAATGGAATAATTGGATTCAGAAAAAGAAAGCTCAAGTCCCAGACAAATCTTGTGTCT	1500
O	y		1190	TCCTTCACGCGTACTTACACCAATATGACCTCTGAAAAATGGCCATCAATAGATGGCTGGA	1244
D	b		1505	TCCTTCACGCGTACTTACACCAATATGACCTCTGAAAAATGGCCATCAATAGATGGCTGGA	1566
O	y		1250	GACACACCAAAAAGTAAA	1266
D	b		1565	GACACACCAAAAAGTAAA	1581
 RESULT 11 US-10-357-930-23179 Sequence 23179, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION: APPLICANT: Schlegel, Robert APPLICANT: Endege, Wilson APPLICANT: Monahan, John TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF TITLE OF INVENTION: HUMAN PROSTATE CANCER FILE REFERENCE: MRI-007BCN CURRENT APPLICATION NUMBER: US/10/357,930 CURRENT FILING DATE: 2003-02-04 PRIOR APPLICATION NUMBER: 09/785,276 PRIOR FILING DATE: 2003-02-16 PRIOR APPLICATION NUMBER: 60/183,319 PRIOR FILING DATE: 2000-02-17 PRIOR APPLICATION NUMBER: 60/189,862 PRIOR FILING DATE: 2000-03-16 PRIOR APPLICATION NUMBER: 60/207,454 PRIOR FILING DATE: 2000-05-25 PRIOR APPLICATION NUMBER: 60/211,314 PRIOR FILING DATE: 2000-06-09 PRIOR APPLICATION NUMBER: 60/219,007					

[illegible]

Db 784 GGGTCAGTGAATAGTCTGATAGTATATAGTACTAATACTGAGATATATCTTCAACA 843
QY 785 ----- 784
Db 844 TTGACTGACACACCAGATATGTCACAATTGTGCTTTTGACCTAATACCTTTACTT 903
QY 785 ----- 784
Db 904 GCTACTGTTCAATGACAAACAGTGAACATCTGGCAATTTGACCTGGAACACTTTGC 963
QY 785 --AGCAGGGCGCACAGAACATCACTGTAAGCAATTTACCGAAGATTGCTCAGAGAGTTC 842
Db 964 CAAGCAAGGGCGCACAGAACATCACTGTAAGCAATTTACCGAAGATTGCTCAGAGAGAT 1023
QY 843 GTCTCAACATGGCTTTGTGACAAAGATTTAAAGATCTTGTGATTTTCAAGATGAAT 902
Db 1024 GTCTCAACATGGCTTTGTGACAAAGATTTAAAGATCTTGTGATTTTCAAGATGAAT 1083
QY 903 AACATTGATGAAAGAACTGTTGAATCTTACAAAAGAAAGTCTGGCTGATGATTTGAA 962
Db 1084 AACATTGATGAAAGAACTGTTGAATCTTACAAAAGAAAGTCTGGCTGATGATTTGAA 1143
QY 963 ATTGAATCTCTAGAGCTGCGTAGTAAAGTCTGAGGAAATTTGAAGACTCAGAGCAAG 1022
Db 1144 ATTGAATCTCTAGAGCTGCGTAGTAAAGTCTGAGGAAATTTGAAGACTCAGAGCAAG 1203
QY 1023 GTTAAATCCCTTTCTTCAGGAATTCCTGATGATTTATATGTCATTAATAGTAAAGCTT 1082
Db 1204 GTTAAATCCCTTTCTTCAGGAATTCCTGATGATTTATATGTCATTAATAGTAAAGCTT 1263
QY 1083 ATGAAAGATCCGCTCATTCGCATCAGATGCGTATTCATATGTAAGAAAGAAAGTAAAT 1142
Db 1264 ATGAAAGATCCGCTCATTCGCATCAGATGCGTATTCATATGTAAGAAAGTAAAT 1323
QY 1143 TGGATCAGCAAAAAGAAAGTACAGATCCCATGACAAATTTTCTTCTTACGGGTA 1202
Db 1324 TGGATCAGCAAAAAGAAAGTACAGATCCCATGACAAATTTTCTTCTTACGGGTA 1383
QY 1203 CTTCACCAAAATGAGCTCTGAAATAGGCCATCATAGATGCTGGAGACACCAAAAG 1262
Db 1384 CTTCACCAAAATGAGCTCTGAAATAGGCCATCATAGATGCTGGAGACACCAAAAG 1443
QY 1263 TAAA 1266
Db 1444 TAAA 1447

RESULT 12
US-10-357-930-29046
Sequence 29046, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357, 930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785, 276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183, 319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189, 862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207, 454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211, 314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219, 007

QY 99 CAAATTAAGAACATGGTGAACATGATTCACACATTAGCTGATCATGTCGACGATGTCAC 158
Db 4 CAAATTAAGAACATGGTGAACATGATTCACACATTAGCTGATCATGTCGACGATGTCAC 63
QY 159 TGCTGACCTTCTCTTTTCCCTCTTGCTGCTACTTCTCTTGGACAAACAAATTCGCTG 218
Db 64 TGCTGACCTTCTCTTTTCCCTCTTGCTGCTACTTCTCTTGGACAAACAAATTCGCTG 123
QY 219 TACTGTTACGTACCTTTACTGACATGTCACATTTCTCCATTTGAATTTCTACTTACT 278
Db 124 TACTGTTACGTACCTTTACTGACATGTCACATTTCTCCATTTGAATTTCTACTTACT 183
QY 279 GTCCATGCTGCTGTTCTTCTCCCTTCCAGGACATATTTGGCATTCGTTCAACAGATGCT 338
Db 184 GTCCATGCTGCTGTTCTTCTCCCTTCCAGGACATATTTGGCATTCGTTCAACAGATGCT 243
QY 339 ACCACTGCTCTATGAAATAGTAAATGACAGATGCTGACATGTCGACATGTCGACATGCT 398
Db 244 ACCACTGCTCTATGAAATAGTAAATGACAGATGCTGACATGTCGACATGTCGACATGCT 303
QY 399 GCGAGCCCTGTGAGGTTTGGCAATTTTCCAGACTCCACGCTGTTTGGCATTCAGGGCA 458
Db 304 GCGAGCCCTGTGAGGTTTGGCAATTTTCCAGACTCCACGCTGTTTGGCATTCAGGGCA 363
QY 459 GCTGATGAAACGTGGTTTGTGAAATGACAGATGTCATACAAATTAATATGATGTGTA 518
Db 364 GCTGATGAAACGTGGTTTGTGAAATGACAGATGTCATACAAATTAATATGATGTGTA 423
QY 519 GTTAAAGATGCTCTTGGCGGATGTCATTTTCTCTAATGAAAGCTTTTGTGACT 578
Db 424 GTTAAAGATGCTCTTGGCGGATGTCATTTTCTCTAATGAAAGCTTTTGTGACT 483
QY 579 GGCTCTCATGTCGATTTTAAACAGTGTGATTAATAAGTGTCTGATAGTAA 638
Db 484 GGCTCTCATGTCGATTTTAAACAGTGTGATTAATAAGTGTCTGATAGTAA 543
QY 639 AAAGCATGATCTTGAATTAACCTGCTGATTTTCTTCAAGGACATTTCTGATGGA 698
Db 544 AAAGCATGATCTTGAATTAACCTGCTGATTTTCTTCAAGGACATTTCTGATGGA 603
QY 699 GAAAGAGTCTTCAGTTTTCGACTGCGATGATGTCAGATTTCCAGATTCAGATTC 758
Db 604 GAAAGAGTCTTCAGTTTTCGACTGCGATGATGTCAGATTTCCAGATTCAGATTC 663
QY 759 TGGATTTCTTTTAAACCATATCTT----- 784
Db 664 TGGATTTCTTTTAAACCATATCTTAAAGTTGAATTAATAATAAGTACATGAGT 723
QY 785 ----- 784
Db 724 GGGCACTGTCCTGCTTCTGCTTCTTCCCATGATGGGACAGATGCTAGTCTCA 783
QY 785 ----- 784

PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255, 281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FaSeq for Windows Version 4.0
SEQ ID NO 29046
LENGTH: 1996
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994,
LOCATION: 1995, 1996
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-29046

Query Match 69.1%; Score 878.8; DB 21; Length 1996;
Best Local Similarity 80.7%; Pred. No. 2,6e-245;
Matches 1166; Conservative 0; Mismatches 2; Indels 276; Gaps 1;

Db 784 GGGTCAGTGGATAGTCTGTATAGTATATAGTACTAATACTGAGAAATATATCTTACACACA 843
Qy 785 ----- 784
Db 844 TTGACTGACGACACAGGATATGTGCAACATTTGCTTTTGACCTTAATACCTTTTACTT 903
Qy 785 ----- 784
Db 904 GCTACTGCTTCATATGACCAAAAACAGTGAACATCTGGCAATTTGACTGGAAACACTTGGC 963
Qy 785 --AGCAAGGGCGACAGAAATCAGCTGAGCAATTTACGAAAGATTTGGTCAGAGAGATC 842
Db 964 CAAGCAAGGGCGACAGAAATCAGCTGAGCAATTTACGAAAGATTTGGTCAGAGAGAT 1023
Qy 843 GTCCTCAACATAGGCTTTGTGCAAGAAATTTAAAGATCTTGTGGTATTTTCAAGATGAT 902
Db 1024 GTCCTCAACATAGGCTTTGTGCAAGAAATTTAAAGATCTTGTGGTATTTTCAAGATGAT 1083
Qy 903 AACATGATGGAAGAAAGCTGTAATCTTACAAAAGAAAGCTGGCGATGATTTGAAA 962
Db 1084 AACATGATGGAAGAAAGCTGTAATCTTACAAAAGAAAGCTGGCGATGATTTGAAA 1143
Qy 963 ATTGAATCTCTAGAGACTGCGTAGTAAAGTCTGAGAAATTTGAAGACTCAGAGACCAAG 1022
Db 1144 ATTGAATCTCTAGAGACTGCGTAGTAAAGTCTGAGAAATTTGAAGACTCAGAGACCAAG 1203
Qy 1023 GTTAAATCCCTTTCTTCAAGAAATCTCTGAGAAATTTATATGCTCAATTAAGAACTT 1082
Db 1204 GTTAAATCCCTTTCTTCAAGAAATCTCTGAGAAATTTATATGCTCAATTAAGAACTT 1263
Qy 1083 ATGAAATATCCGCTCATCGCATCGATGCGATTCATATGAAAGAAAGCAATGGAAT 1142
Db 1264 ATGAAATATCCGCTCATCGCATCGATGCGATTCATATGAAAGAAAGCAATGGAAT 1333
Qy 1143 TGCATCAGCAAAAAGAAAGCTGACAGTCCCATGACAAATCTTCTTCTTCCCTCAGCGTA 1202
Db 1324 TGCATCAGCAAAAAGAAAGCTGACAGTCCCATGACAAATCTTCTTCTTCCCTCAGCGTA 1383
Qy 1203 CTTACACCAATATAGGACTCTGAAAAATGGCCATCAATATAGTGGCTGAGACACACCAAAAG 1262
Db 1384 CTTACACCAATATAGGACTCTGAAAAATGGCCATCAATATAGTGGCTGAGACACACCAAAAG 1443
Qy 1263 TAAA 1266
Db 1444 TAAA 1447

RESULT 13

US-10-077-111-14
; Sequence 14, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Todderud, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-4114US2
; CURRENT APPLICATION NUMBER: US/10/077,111
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: RET 16.3 splice variant
US-10-077-111-14

Query Match 69.0%; Score 877.8; DB 14; Length 1908;
Best Local Similarity 77.9%; Pred. No. 4.9e-245;
Matches 1253; Conservative 0; Mismatches 2; Indels 354; Gaps 2;
Qy 12 TCACCTGCGGCGACGATGACCGGACCGCGGACCTTGAGAGGAGATCCCGGCG 71
Db 37 TCACCTGCGGCGACGATGACCGGACCGCGGACCTTGAGAGGAGATCCCGGCG 96
Qy 72 CCCCCGCTCCTGCAAGGCTGTTTTCTTCAATTAAGAAATGTTGAACATGATTCACACA 131
Db 97 CCCCCGCTCCTGCAAGGCTGTTTTCTTCAATTAAGAAATGTTGAACATGATTCACACA 156
Qy 132 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
Db 157 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 216
Qy 192 TGCTCCTTGGACAAACAAATTCGCTGATCTGTTACGTGACCTTTACTGAACCTGCCAT 251
Db 217 TGCTCCTTGGACAAACAAATTCGCTGATCTGTTACGTGACCTTTACTGAACCTGCCAT 276
Qy 252 TCTTCATTTGAAGTTTCACTTACCTATGCTGTCACCTGCTGCTTTTCTCCCTCAGACAT 311
Db 277 TCTTCATTTGAAGTTTCACTTACCTATGCTGTCACCTGCTGCTTTTCTCCCTCAGACAT 336
Qy 312 ATTTTGGCATCGTGTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
Db 337 ATTTTGGCATCGTGTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 396
Qy 372 ATGCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
Db 397 ATGCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456
Qy 432 GACTCCAGCTGTTGGCATCAGGGGACGCTGATGAACTGTGTTTGTGGAATGACAG 491
Db 457 GACTCCAGCTGTTGGCATCAGGGGACGCTGATGAACTGTGTTTGTGGAATGACAG 516
Qy 492 TCATACCAATTAATATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
Db 517 TCATACCAATTAATATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
Qy 552 TCTCCTAATGGAAGCTTCTTGTGATCAGGCTCCTCATGATGATGATGATGATGATGATGAT 611
Db 577 TCTCCTAATGGAAGCTTCTTGTGATCAGGCTCCTCATGATGATGATGATGATGATGATGAT 636
Qy 612 GATTAATATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
Db 637 GATTAATATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
Qy 672 TTTTCTTCAAGCAGCTTCTGATGAGAAACAGGCTTCAAGTTTTCGACTGGCATCA 731
Db 697 TTTTCTTCAAGCAGCTTCTGATGAGAAACAGGCTTCAAGTTTTCGACTGGCATCA 756
Qy 732 TGTGTCAGATTTGCCAAGTCAAAATTTGATTTCTTTTACCCATATCTT----- 784
Db 757 TGTGTCAGATTTGCCAAGTCAAAATTTGATTTCTTTTACCCATATCTTATAGTTTT 816
Qy 785 ----- 784
Db 817 GAATTAATAATATAAAGTACAGTGAAGGACAGTGTCTCTCTTCTGCTTGTCTTTT 876
Qy 785 ----- 784
Db 877 TCCCATGATGGCAGATGCTAGTCTCAGGCTCAGTGATAGTCTGCTCATATATATGAT 936
Qy 785 ----- 784
Db 937 ACTAATAGTGAATATATCTTCAACATGATGATGATGATGATGATGATGATGATGATGAT 996
Qy 785 ----- 784
Db 997 GCTTTTGACCTATATACCTTTTACTTGTCTAGTGTCAATGACAAACAGTGAAATC 1056

QY 785 -----AGCAAGCGCAGACAATCAGCTGAAGCAA 815
Db 1057 TGGCAATTTGACCTGGAAACATTTTGGCAAGCAAGGGGCAACAGATCTGAGGAA 1116
QY 816 TTTACCGAAGATTGGTCAGAGAGCTGTCTCAACATGGCTTTGTGCAACAAGTTTAAA 875
Db 1117 TTTACCGAAGATTGGTCAGAGAGAGCTGTCTCAACATGGCTTTGTGCAACAAGTTTAAA 1176
QY 876 GATCTGTGGTATTTTCAAGATGAATTAACATTTGATGGAAGAAAGACTGTGAATCTTACA 935
Db 1177 GATCTGTGGTATTTTCAAGATGAATTAACATTTGATGGAAGAAAGACTGTGAATCTTACA 1236
QY 936 AAGAAAGCTGGCTGATGATTTGAAATTTG----- 966
Db 1237 AAGAAAGCTGGCTGATGATTTGAAATTTGAGAGTCTCTGCGATGATGCTC 1296
QY 967 -----AATCTTAAGA 977
Db 1297 ACTGACAGCTTCAACCTCTGGGCTCAAGTATCTCTCACTGCGCTCAATCTTAAGA 1356
QY 978 CTGCTAGTAAAGTGTGAGAAATTTGAAGAGCTCAGACCAAGGTTAAATCGCTTCT 1037
Db 1357 CTGCTAGTAAAGTGTGAGAAATTTGAAGAGCTCAGACCAAGGTTAAATCGCTTCT 1416
QY 1038 TCAGGAATTCCTGATGAATTTATATGTCAATACTAGAGAACTTATGAAAGATCCGCTC 1097
Db 1417 TCAGGAATTCCTGATGAATTTATATGTCAATACTAGAGAACTTATGAAAGATCCGCTC 1476
QY 1098 ATGCAATCAGATGCTATTTATATGAAAGCAATGGAATTTGATCAGCAAAAG 1157
Db 1477 ATGCAATCAGATGCTATTTATATGAAAGCAATGGAATTTGATCAGCAAAAG 1536
QY 1158 AAACGTACAAGTCCCATGACAAATCTGTCTTCTTCAAGGTACTTACCAAAATAGG 1217
Db 1537 AAACGTACAAGTCCCATGACAAATCTGTCTTCTTCAAGGTACTTACCAAAATAGG 1596
QY 1218 ACTCTGAAAATGGCCATCAATAGATGGCTGGAGACACCAAAAGTAA 1266
Db 1597 ACTCTGAAAATGGCCATCAATAGATGGCTGGAGACACCAAAAGTAA 1645

RESULT 14
US-10-956-157-10363
; Sequence 10363, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10363
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-10363

Query Match 47.3%; Score 602.2; DB 22; Length 1400;
Best Local Similarity 76.1%; Pred. No. 1,4e-164;
Matches 890; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY 374 GCTGGAGATGATGAACAGGCTAGTGGACAGCCTGTGAGAGTTTGGCAGTTTCCACAGA 433
Db 1 GCTGGAGATGATGAACAGGCTAGTGGACAGCCTGTGAGAGTTTGGCAGTTTCCACAGA 60
QY 434 CTCACGATGTTGGCATTCAGGAGCAGCTGATGGAATGTGTTTGTGAATGACAGT 493
Db 61 CTCACGATGTTGGCATTCAGGAGCAGCTGATGGAATGTGTTTGTGAATGACAGT 120

QY 494 ATCAAAATATATAGATGTAGTGTGTTAAAGATGCTCTTGGCGGACATGCAATTTTC 553
Db 121 ATCAAAATATATAGATGTAGTGTGTTAAAGATGCTCTTGGCGGACATGCAATTTTC 180
QY 554 TCCTAATGGAAGCTTTTGTGCACTGGCTCTCATGTGTGATTTAACTGTGGATGA 613
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QY 614 TAAATGAGGTGTCTGATAGTAAAGAACATGATCTTGGAAATTAACCTGGCTGCA 673
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QY 674 TTCTTCAACCCAGTTTCTGATGAGAAACAGATCTTCAATTTTTCGATGCAATG 733
Db 301 TTCTTCAACCCAGTTTCTGATGAGAAACAGATCTTCAATTTTTCGATGCAATG 360
QY 734 TGGTCAGATTTGCCAAGTCAAAATTTGATTTTCTTTTACCATATCTT----- 784
Db 361 TGGTCAGATTTGCCAAGTCAAAATTTGATTTTCTTTTACCATATCTTAGTTTGA 420
QY 785 ----- 784
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QY 785 ----- 784
Db 481 CCATGATGGCAGATGCTAGTCTCAGAGGTCAATGATTAATGTCATAGTATATGATAC 540
QY 785 ----- 784
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QY 785 ----- 784
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QY 785 -----AGCAAGCGCAGACAGAACATCAGCTGAAGCAAT 817
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Db 901 GAAAAATTGGAAGCTCAGAGCAAGGTTAAATCTTCTTCAAGAAATCTCTGATGAAT 960
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QY 1178 AAATCTTGTCTTCTTCAAGCGGTACTTACACCAATTTGACCTGGAATGCGCATTC 1237
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QY 1238 TAGATGCTGAGACACACCAAAAGTAA 1266
Db 1141 TAGATGCTGAGACACACCAAAAGTAA 1169


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RESULT 15
US-10-077-111-6
; Sequence 6, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Todderud, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-4114US2
; CURRENT APPLICATION NUMBER: US/10/077,111
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: MOUSE
US-10-077-111-6

Query Match      36.5%; Score 464; DB 14; Length 1901;
Best Local Similarity 63.2%; Pred. No. 4,2e-124;
Matches 916; Conservative 0; Mismatches 255; Indels 279; Gaps 2;

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QY 153 GTCACTGCTGCTGCTTCTCTCTTCCCTCTTGCTTACTGCTCTGCTTGAAGAAATTC 212
DB 61 GTAGCTGCTGCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 213 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272
DB 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 273 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332
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DB 241 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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QY 513 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
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DB 541 AGCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 693 GATGAGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
DB 601 GCGGAG--AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
QY 753 AAAATTGATGTTGTTCTTTTACCATATCTT----- 784
```

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DB 658 AAACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
QY 785 ----- 784
DB 718 CTAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
QY 785 ----- 784
DB 778 GCATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
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DB 958 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
QY 837 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
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QY 897 ATGATTAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
DB 1078 GCAAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
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DB 1318 GAAATTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
QY 1197 GCGTAACTTAACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1256
DB 1378 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437
QY 1257 CAATAAGTAA 1266
DB 1438 GAGAAAGTAA 1447
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Search completed: October 25, 2005, 11:11:25
Job time : 2690 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 25, 2005, 01:02:43 ; Search time 2816 Seconds

(without alignments)
5190.582 Million cell updates/sec

Title: US-10-077-111-13

Perfect score: 2047
Sequence: 1 MVKLHRLADHGDVNCACAF.....LTPRLTKMAINRWLETHQK 384

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US10077111/funat_24102005_072846.8180/app_query.fasta_1.583
-DB=EST -QPMT=fastap -SUFFIX=retc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US10077111.@CGN_1.1_2607.@funat_24102005_072846.8180 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_estc1: *
2: gb_estc2: *
3: gb_hic: *
4: gb_estc3: *
5: gb_estc4: *
6: gb_estc5: *
7: gb_estc6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1977	96.6	1770	3	CR607851 full-length
2	1714.5	83.8	1600	3	CR619104 full-length
3	1617	79.0	2027	3	AK011391 Mus muscu
4	1205	58.9	889	1	AL553333 AL553333
5	1203	58.8	941	1	AL533510 AL533510
6	1154	56.4	1010	4	BMS43484 AGENCOURT
7	1043.5	51.0	858	4	B1603184 B1603184
8	1031.5	50.4	792	4	B1821143 B1821143
9	1005	49.1	728	7	CN793033 CN793033

10	975.5	47.7	910	5	B0895162	B0895162 AGENCOURT
11	943.5	46.1	838	4	B1107478	B1107478 B02893815
12	907	44.3	839	7	CK306752	CK306752 SB02035A1
13	883.5	43.2	808	7	CK792250	CK792250 AGENCOURT
14	880	43.0	499	5	BX282729	BX282729 BX282729
15	880	43.0	696	4	B1759505	B1759505 603046888
16	879	42.9	727	7	CK364577	CK364577 AGENCOURT
17	873	42.6	505	1	A1189142	A1189142 qd04a04.x
18	872	42.6	807	1	AL040518	AL040518 DKFZP434G
19	856.5	41.8	817	5	B0961462	B0961462 AGENCOURT
20	854	41.7	718	5	B0356767	B0356767 603475939
21	834	40.7	652	2	B8653743	B8653743 B8653743
22	821	40.1	669	1	AJ726222	AJ726222 AJ726222
23	801	39.1	869	5	B0148588	B0148588 AGENCOURT
24	797	38.9	760	5	B0273077	B0273077 603533394
25	758.5	37.1	965	4	BG769613	BG769613 6027444525
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27	747	36.5	919	5	BQ713478	BQ713478 AGENCOURT
28	746	36.4	791	7	CK603751	CK603751 AGENCOURT
29	739	36.1	682	6	BY710675	BY710675 BY710675
30	725	35.4	768	7	CK846814	CK846814 969364 MA
31	719	35.1	559	4	B1681850	B1681850 461338 MA
32	715	34.9	967	1	AL533462	AL533462 AL533462
33	705	34.4	797	5	BU423666	BU423666 603961466
34	700	34.2	764	4	BG619844	BG619844 602618021
35	698.5	34.1	767	7	CN526819	CN526819 UI-M-HB0-
36	691	33.8	723	9	CE487278	CE487278 ligf-g88-
37	690	33.7	632	4	BG624489	BG624489 B0624489
38	677	33.1	626	4	BG562985	BG562985 602581153
39	673.5	32.9	447	1	AA118718	AA118718 mp57c07.r
40	668.5	32.7	1042	4	BG435096	BG435096 602507104
41	662.5	32.4	829	7	CO567478	CO567478 AGENCOURT
42	662	32.3	463	7	CN407189	CN407189 170006000
43	662	32.3	897	5	B0964199	B0964199 AGENCOURT
44	657	32.1	1010	3	BC039804	BC039804 Mus muscu
45	648	31.7	699	1	AJ726210	AJ726210 AJ726210

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Full-length cDNA clone CS0DN004Y15 of Adult brain of Homo sapiens (human).
ACCESSION CR607851 GI:50488658
VERSION CR607851.1
KEYWORDS HTC; cDNA; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1. (bases 1 to 1770)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@life.technet.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue
Genoscope.
2 (bases 1 to 1770)
REFERENCE Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cnm.fr - Web: www.genoscope.cnm.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. 1770
/organism="Homo sapiens"

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Alignment Scores:	
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Score:	1977.00
Percent Similarity:	80.25%
Best Local Similarity:	80.25%
Query Match:	96.58%
DB:	3
	Gaps: 1

2.93e-190 Length: 1770

1977.00	Matches:	382
80 353	Conservative:	0

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80.25%
conservative: 0
mismatches: 2

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96.58%	Indels:	92
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	3	1
Gaps:		

US-10-077-111-13 (1-384) x CR607851 (1-1770)

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QY	21	ScrPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg	40
Db	228	TCCTTTTCCTCTTGCGTCACTTGCTCCCTTGGCAAAACAATTGCGCTTACCTCGTTAGCT	287
QY	41	AspPheThrGluLeuProH1sSerProLeuLysPheH1sThrTyrAlaValHisCysCys	60
Db	288	GACCTTACTGAACTGGCCACATTCCTCCATGTGAAGTTCATACCTTAAGCTGCACACTGCTGC	347
QY	61	CysPheSerProSerG1yH1sIleLeuAlaSerCysSerThrAspG1yThrThrValLeu	80
Db	348	TGTTTCTCCCTTCACGACATATTTTGGCATGCTGTTCAACAGATGATACACTGTCTTA	407
QY	81	TrpAsnThrGluAsnG1yGlnMetLeuAlaValMetGluGlnProSerG1ySerProVal	100
Db	408	TGGAAATCTGAAAAATGGACAGATGCTGGCAGATGGAACAGCCATAGTGGCAGCCCTGTG	467
QY	101	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerG1yAlaAlaAspG1yThr	120
Db	468	AGGGTTTGCCAGTTTCCCAACACTCCACGATGTTTGGCATCAGGGGGCAGCTGATGAACT	527
QY	121	ValValLeuThrPAsnAlaGlnSerTyrLysLeuTyrArgCysG1ySerValLysAspG1y	140
Db	528	GTGGTTTGTGGAAATGCACAGTCATACAAATATATATAGATGCTGAAGTTAAAGATGGC	587
QY	141	SerLeuAlaAlaCysAlaPheSerProAsnG1ySerPhePheValThrGlySerSerCys	160
Db	588	TCCCTGGGGGCAATGGCAATTTTCTCTTAATGGAACCTTCTTGGTCACTGGCTCCCACTGT	647
QY	161	G1yAspLeuThrValTrpAspAspLysMetArgCysLeuH1sSerGluLysAlaHisAsp	180
Db	648	GGTGATTTAACAGTGTGGGATGATTAATGAAGTGTCCGCATAGTGAATAAAGCACATAT	707
QY	181	LeuG1yIleThrCysCysAspPheSerSerGlnProValSerAspG1yGluGlnG1yLeu	200
Db	708	CTTGGAAATTACTGCTGGCATTTTCTTCACAGCAGATTTCTGATGGAGAAACAAGCTTT	767
QY	201	GlnPhePheArgLeuAlaSerCysG1yGlnAspCysGlnValLysIleTrpIleValSer	220
Db	768	CAGTTTTTTCACCTGGCATCATGTGGTCAGATGGCCAAGTCAAAATTGTGATGTTTCT	827
QY	221	PheThrHisIleLeu-----	225
Db	828	TTTACCCCATCTTAAGTTTGAATTAAATATATAAAGTACACTGATGGGCACGTGTCT	887
QY	225	-----	225
Db	888	CCTGTTCTGGCTGTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGGAT	947
QY	225	-----	225
Db	948	AAGTCTGTCATAGTATATGATACATACTAGAAATATATCTTACACACATTGACTCAGAC	1007

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/plasmid="PCWSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 1 48e-163 Length: 1600
Score: 1714.50 Matches: 335
Percent Similarity: 70.38% Conservative: 0
Best Local Similarity: 70.38% Mismatches: 2
Query Match: 83.76% Indels: 139
DB: 3 Gaps: 2

US-10-077-111-13 (1-384) x CR619104 (1-1600)

1 MetValIysLeuIleHsIsthLeuAlaSpHsGlyAspAspValAsnCySAspAlaPhe 20
112 ATGGTGAAGCTGATTCACACATTCAGTGCATGTCAGTGCATGTCAGTGCCTTC 171
21 SerPheSerLeuLeuAlaThrCySerLeuAspLysThrIleAsgLeuTySerLeuArg 40
172 TCCCTTTCCTCTGGCTACTTGTCTCTGGACAAACAATTCGCTGTACTCTGTACGT 231
41 AspPheThrGluLeuProHsSerProLeuLysPheHsIsthTyAlaValHsCySAsp 60
232 GACTTTCAGTACGTCACATTCCTCATTCAGTGAAGTTTCATACCTATGCTGCACAGTGC 291
61 CysPheSerProSerGlyHsIleLeuAlaSerCySerThrAspGlyThrThrValLeu 80
292 TGTTCCTCCCTTCAGGACATATTTGGCATCGTGTTCACAGATGTCACACAGTCTCTA 351
81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
352 TGGATATCTGAAATGACAGATCTGTCAGTGAAGACCTAGTCGACAGCCCTGTG 411
101 ArgValCySglnPheSerProSerProSerThrCySerLeuAlaSerGlyValAlaAspGlyThr 120
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121 ValValLeuThrPAsnAlaGlnSerTyLysLeuTyArgCySglnSerValLysAspGly 140
472 GTGCTTTTGTGGATGACACATTCATACAAATTATATATAGTGTGAAGTAAAGATGC 531
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532 TCCCTGGCGCATGTGCATTTCTCTAATGGAAGCTTCTTGTCACTGGCTCTCATGT 591
161 GlyAspLeuThrValITrpAspAspLysMetArgCySLeuHsIsthSerGlyLysAlaHsAsp 180
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181 LeuGlyIleThrCySAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
652 CTTGGAAATTAACCTGCTGCGATTTTCTTCAACAGCAGTTTCTGATGGAGAACAAAGTCTT 711
201 GlnPhePheAlaGlyLeuAlaSerCySglnGlnAspCySglnValLysIleTrpIleValSer 220
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221 PheThrHsIsthLeu----- 225
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225 ----- 225
832 CCTGTTTCGGCTGTGCTTTTCCATGATGGCGAGATGCTAGTCTCAGGGTCAGTGAT 891
225 ----- 225
892 AAGTCTGTCATAGTATATGATACTAATACTGAGAAATATATCTTCAACATGAGTCAAGCAC 951

225 ----- 225
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226 ----- AlaArgArg 228
1012 ATGACAAACACATGACATCTGCGCAATTGACCTGGAAACACTTTCGCCAAGCAGCGGC 1071
229 ThrGluHsIsthLeuLysGlnPheThrGluAspTrpSerGluGluValAlaSerThrTrp 248
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1132 CTTTGTGACACAGATTTAAAGATCTTCTGTGATTTTTCAGATGATTAACATTGATGCA 1191
269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspLeuLysIleGluSerLeu 288
1192 AAAGAACTGTGATCTTACAAAGAAAGTCTGCTGATGATTTGAAAAAT----- 1242
289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
1242 ----- 1242
309 SerSerGlyIleProAspGluPheIleCySProIleThrArgGluLeuMetLysAspPro 328
1242 ----- 1242
329 ValIleAlaSerAspGlyTySerTyGluLysGluAlaMetGluAsnTrpIleSerLys 348
1243 -----GATGCTATTTCATATGAAAAAGAACCAATGAAAAATTTGATCAGCAAA 1290
349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValIleThrProAsn 368
1291 AAGAAAGTACCAATCCCATGACCAAAATCTTGTCTTCTTCAGGCGGATTAACCAAAAT 1350
369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHsGlnLys 384
1351 AGGACTCTGAAATGCGCATCATATGATGCTGAGACACACCAAAAG 1398

RESULT 3
AK011391
LOCUS
DEFINITION
MUS musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610014P08 product:hypothetical SAM domain
(Ser/ile alpha motif)/Modified RING finger domain/G-protein beta
WD-40 repeats containing protein, full insert sequence.
AK011391
VERSION
AK011391.1 GI:12847483
KEYWORDS
HTC; CAP trapper.
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
PUBMED
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M.,
Sun, Y., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

[illegible]

Db	823	ATTACCGCTGCTTAGAGCTTTGAATTAATAATATAAAGCACATPAGTGGCATTGGCC	882
Qy	222	-----	222
Db	883	CCTGCTTCGCGCTGCTTTTTCATCATGATGAAAGATGCTTGATCGGGTGCATGTGAT	942
Qy	223	-----	228
Db	943	AAATTCGTCAATCATATCATGATGATGGCCCTCAGAGTGTGTACACACCGCTGATCAGCAT	10020
Qy	229	ThrluHts-----	231
Db	1003	ACCAAGTATGTAGACATCTTGCCGTTTGACACCAACACTCTCTTAATTGCTACTGTTTCA	10632
Qy	231	-----	231
Db	1063	ATGACAAAGACAGTGAACATTTGGCAGTTTGACCTGGAACACCTTGCCAAAGAAAGCATG	11222
Qy	232	-----GlnLeuLyvGlnPheThrGlnAspTrpSerGluGluValValSerThrTrpLeu	249
Db	1123	AACGACCCGCTGAAACATTTCTACGTGAAGAAATGCTCAGAGGAGATGTCCTCCGTGGCTT	11822
Qy	250	CysIaGlnAspLeuLyvAspLeuValGlyIlePheLyvMetAsnAsnIleAspGlyLyv	269
Db	1183	CGTGTCAAGCGCTTGGAGACCTGCTCGCATTTTTCAGGGCAACACATCGATGGGAA	12422
Qy	270	GlnLeuLeuAsnLeuThrLyvGluSerLeuValAspAspLeuLyvIleGluSerLeuGly	289
Db	1243	GAATCTATTGCATCTCACAAAGAAAGCTGGCTGTGTATTTGAAATTCGATCTTAGGG	13020
Qy	290	LeuArgSerLyvValLeuArgLyvIleGluGluLeuArgThrLyvValLyvSerLeuSer	309
Db	1303	CTGCGCAGCAAAAGCTCTGAGAGATTTGAAAGCTCAGGGCCAAAGATGATTCCTCTCT	13622
Qy	310	SerGlyIlePProAspGlnPheIleCysProIleThrArgGluLeuMetLyvAspProIa	329
Db	1363	TCCGGAATCCTTGACGAGTTATCTGCCCCAATPACCAAGAACTCATTAAGAACCCGCTC	14222
Qy	330	IleAlaSerAspGlyTyrSerTyrgluysgluIaMetGluAsnTrpIleSerLyvLyv	349
Db	1423	ATGCGATCAGATGGCTACTCTCTACGAGAGAGAAAGAAAGCTGATCCACAAGAG	14822
Qy	350	LyvArgThrSerPromeThrAsnLeuValLeuProSerAlaValLeuThrProAsnArg	369
Db	1483	AAGGTAACGAGCCCATACAAATTTGGCTCTCCCTTACGTGTACTAACCCCAACAGG	15422
Qy	370	ThrluysMetAlaIleAsnArgTrpLeuGlnThrHsgLys 384	
Db	1543	ACACTGAAGATGCCATCAACCGATGGCTGGAGACGACGAGAAG 1587	
RESULT 4			
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DEFINITION	AL553333 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		EST 30-MAR-2004
ACCESSION	AL553333		
VERSION	AL553333.3	GI:45858102	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 889)		
JOURNAL	Li, W.B., Gruber, C., Jesssee, J., and Polayars, D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	On Feb 15, 2001 this sequence version replaced gi:31275147.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequenage		
	2 rue Gascon Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	1st strand cDNA was primed with a NotI-oligo(dt) primer. Five primam		
	end enriched, double-strand cDNA was digested with Not I and clone		

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1653.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdnafs=CS0D1075DAD04Q16c-1653.r>.

Location/Qualifiers

1..889

FEATURES

source

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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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Alignment Scores:

Pred. No.:	5.48e-112	Length:	889
Score:	1205.00	Matches:	222
Percent Similarity:	99.12%	Conservative:	2
Best Local Similarity:	98.23%	Mismatches:	1
Query Match:	58.87%	Indels:	1
DB:	1	Gaps:	0

US-10-077-111-13 (1-384) x AL553333 (1-889)

QY	1	MetValLysLeuLeuIleHisThrLeuAlaAspHisGlyAspAspValAlaAspCysAlaPhe	20
Db	112	AtGctGAACtGATGATTCACATTAAGTGTGCGATGCTGACATGCTGAGCTTC	171
QY	21	SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTySerLeuArg	40
Db	172	TCTTTTCCCTCTGGCTACTTGCTCTTGGAACAACAATTCGCTGTACTGTTACGT	231
QY	41	AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyAlaValHisCysCys	60
Db	232	GACTTAACTGCACTGCCACATTTCTCATTAAGATTCACTTAAGCTGTCACCTGCTG	291
QY	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
Db	292	TGTTTCTCCCTTCAGAGACATATTTTGGCATGCTGTTCAACAGATGATACCATGCTCTA	351
QY	81	TyrAsnThrGluAsnGlyGlnMetLeuAlaValMetGlnInProSerGlySerProVal	100
Db	352	TGGAAATACGAAAAATGACAGATGCTGGCAGCATGCAACAGCTACGAGCAGCCCTGTG	411
QY	101	ArgValCysGln-PheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyTh	120
Db	412	AGGGTTGGCAGTTTTTCCCGAGCTCCACGTTGTGGCAATCAGAGGCAGCTGATGGAAC	471
QY	120	ValValLeuThrPasnAlaGlnSerTyLysLeuTyArgCysGlySerValLysAspGly	140
Db	472	TGTGCTTTGTGGAAATGCACACTCATACAAATTATATGATCTGTACTGTAAAGATCG	531
QY	140	YSerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCy	160
Db	532	CTCTCTGGGGGCGATGCGCTTTTCTTCCTAAATGGAAGCTTCTTTGTCACTGGCTCTCATG	591
QY	160	SglYAspLeuLeuThrValTyrPaspAspLysMetArgCysLeuHisSerGlnGlyValAlaHis	180
Db	592	TGGTGATTTATCATGCTGTGGCATGATPAATAATGAGTGCTGTGATATGTGAATAAGCATATGA	651
QY	180	PheGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLe	200
Db	652	TCTTGGAAATTAACCTGCTGCATTTTCTTTCACAGCCAGTTCTGATGAGAAACAAGCTCT	711
QY	200	uGlnPhePheAspLeuAlaSerCysGlyGlnAspCysGlnValLysIleThrPheValSer	220
Db	712	TCAAGTTTTTGCATGCGATCATGATGGTAAAGATTGCCAAATCAAAAATTGGATTGTTTC	771

Qy	220	rphethrHsiIleLeu	225
Db	772	TTTtACCAATAtCTTA	787
RESULT 5			
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LOCUS	941 bp	mRNA	linear
DEFINITION	AL533510 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone		EST 24-MAR-2004
	CSDNDN004YV15 5-PRIME, mRNA sequence.		
ACCESSION	AL533510		
VERSION	AL533510.3	GI:45708442	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 941)		
AUTHORS	Lt.W.B., Gruber,C., Jeessee,J. and Polayzes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On Feb 13, 2001 this sequence version replaced gi:31260591.		

Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: segre@genoscope.cns.fr Web : www.genoscope.cns.fr
185 strand cDNA was primed with a NotI-oligo (dT) primer. Five primer
end enriched, 1 double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1653.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna/seq/CE0DDND04/CE08QPltc=1653.r>

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FEATURES
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                /dev_stage="adult"
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                /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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Alignment Scores:	
Pred. No.:	9,596-112
Score:	1203.00
Percent Similarity:	98.22%
Best Local Similarity:	97.78%
Query Match:	58.77%
DB:	1
	Gaps:
	0

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Dd	167	ATGGACACACGATTCAACACTTACTCATCTAGTCGCATGTCCATCGCTGTTGCCCTTC	226
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Dd	227	TCTCTTTCCCTGGCTACTTGCTGCCTTGGACAAMAAATTCGGCTCTTMCCTGTTACTGT	286
OY	41	AspPheThrGluLeuProHissSerProLeuLysPheHisThrTyralValHisCysCys	60
Dd	287	GACTTTACTGAACCTCCACACTTCTCATTTGAAGTTTCACTTAAGCTGTCCACACGCTGCC	346
OY	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80

Db	347	TGTTTCTCCCTTCAGGACATATTTTGGCATTCGTTTCACACAGATGGATCACACTGTCTTA	406
OY	81	TrypanthrGlubangIylGImetLeuAlaValMetCluGlnProSerGlySerProVal	100
Db	407	TGGAAATCTGCAAAATGGACAGATCTGGCAGTGATGGAAACAGCCTTACGTGCAGCCCTGTG	466
OY	101	ArgAlaValGlnPheSerProAspSerThrCysAlouAlaSerGlyAlaAlaAspGlyThr	120
Db	467	AGGGTTGGCCAGTTTCCCGAGACTCCACGGTTGGCATTCAGGGGACGCTGAAGAACT	526
OY	121	ValValLeuTrypanAlaGlnSerTryLeuLeuTryArgCysGlySerValIlyAspGly	140
Db	527	GTGGTTTGTGGATATGCACACAGGCATACMAATTAATATGATGTGTACTGTTAAAGATGGC	586
OY	141	SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	587	TCCTTGGCGGCGMTGTGCATTTTCTCTAATGGAGCTTCTTTCACATGGCTCTCTCATGT	646
OY	161	GlyAspLeuThrValITrypanAspGlyMetCArgCysLeuHisSerGlyIuLysAlaHisAsp	180
Db	647	GGTAAATTTAACAGGTGGGATGATAAATAGAGGTGTGCATATGATGAATAAAGACATGAT	706
OY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu	200
Db	707	CTTGGAAATTACCTGCTGTCGATTTTTTCTTCACAGCCAGTTTCTGATGGAGAACAGGCTTT	766
OY	201	GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrioIlyAlaSer	220
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OY	221	PheThrHisIleLeu	225
Db	827	TTTACCATATCTTA	841

RESULT	6
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LOCUS	
DEFINITION	BMS43484 1010 bp mRNA linear EST 20-FEB-2002
ACCESSION	AGNCNCOURT 6492519 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5765727
VERSION	5', mRNA sequence.
KEYWORDS	BMS43484 BMS43484.1 GI:18773915
SOURCE	EST.
ORGANISM	Homo sapiens (human)
TITLE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarcheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1010) NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

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FEATURES
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DNA Sequencing by: Agencourt Bioscience Corporation
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
Tissue Procurement: Invitrogen
Email: cgapbs@wmtall.nih.gov

```

(destroyed); Site 2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

ORIGIN

Alignment Scores:

Pred. No.:	1.07e-106	Length:	1010
Score:	1154.00	Matches:	222
Percent Similarity:	96.96%	Conservative:	1
Best Local Similarity:	96.52%	Mismatches:	2
Query Match:	56.38%	Indels:	5
	4	Gaps:	0

US-10-077-111-13 (1-384) x BM543484 (1-1010)

Qy	1	MetValIysLeuIleHsThrLeuAlaAspHisGlyAspAspValaIasnCyCysAlaPhe	20
Db	186	ATGTTGAAACGATTCACACATTCAGTATCATGTGACATGTCACACTGCTGCTTC	245
Qy	21	SerPheSerLeuLeuAlaThrCysSerLeuAspIysThrIleArgLeuTyrSerLeuArg	40
Db	246	TCCTTTCCCTCTGGCTACTGCTCTTGGACAAACATTCGCTGTACTCGTTAGCT	305
Qy	41	AspPheThrGluLeuProHisSerProLeuIysPheHisThrTyrAlaValHisCysCys	60
Db	306	GACCTTACTGAACTGCCACATTCCTCAATGAAATTCATACCTTACCTGCTGCTGCTGC	365
Qy	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
Db	366	TGTTTCTCCCTTCAAGACATATTTTGGCATGTGTTCAACAGATGGTACCACTGCTTA	425
Qy	81	TyrPanthrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	100
Db	426	TGGAATCTGAAATATGACACATGCTGCGACATGGAACAGCCATGCGCAGCCCTGTG	485
Qy	101	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr	120
Db	486	AGGCTTTCGCCAGTTTCCCGACCTCCACGTGTTGGCATGAGGCGCAGCTGATGAACT	545
Qy	121	ValValLeuThrAspAlaGlnSerTyrIleLeuTyrArgCysGlySerValIysAspGly	140
Db	546	GTTGTTTGTGGATTCACACATTCATACAAATTAATAGATGGTATGTTAAAGATGGC	605
Qy	141	SerLeuAlaIaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	606	TCCTTGGGGCATGTGCATTTCTCTTAATGAAGCTTTCTGTCACTGGCTCCCTCATGT	665
Qy	161	GlyAspLeuThrValTyrAspAspIysMetArgCysLeuHisSerGluIysAlaHisAs	180
Db	666	GGTATTTTAAACAGTCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT	725
Qy	180	PleuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyL	200
Db	726	TCTTGAATTAACCTGCTGCGATTTTCTTCCAGCGGATTTCTGATGGAAGAAAGGCTC	785
Qy	200	eu-glnPhePheArgLeuAlaSerCysGlyGlnAsp-CysGlnValIysIleTyrIleV	219
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ACCESSION	BI603184		

VERSION BI603184.1 GI:15496123
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT
Contact: Robert Straubeberg, Ph.D.
Email: cgaops-remail.nih.gov
Tissue Procurement: Miklos Palkovics, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shizaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM11763 row: h column: 08
High quality sequence stop: 756.

FEATURES

source

Location/Qualifiers
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/note="Organ: brain; Vector: pBluescriptRP (modified pBluescript KS+); Site: 1: BamHI; Site 2: SalI-XhoI (gcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTAA-3', size-selected for average insert size 2.3 kb and normalized to R0F 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.54e-95	Length:	858
Score:	1043.50	Matches:	215
Percent Similarity:	90.79%	Conservative:	2
Best Local Similarity:	89.96%	Mismatches:	13
Query Match:	50.98%	Indels:	9
DB:	4	Gaps:	1

US-10-077-111-13 (1-384) x BI603184 (1-858)

Qy	1	MetValIysLeuIleHsThrLeuAlaAspHisGlyAspAspValaIasnCyCysAlaPhe	20
Db	151	ATGTTGAAACGATTCACACATTCAGTATCATGTGACATGTCACACTGCTGCTTC	210
Qy	21	SerPheSerLeuLeuAlaThrCysSerLeuAspIysThrIleArgLeuTyrSerLeuArg	40
Db	211	TCCTTTCCCTCTGGCTACTGCTCTTGGACAAACAAATTCCTGCTACTCGTTAGCT	270
Qy	41	AspPheThrGluLeuProHisSerProLeuIysPheHisThrTyrAlaValHisCysCys	60
Db	271	GACTTACTGAACTGCCACATTCCTCAATGAAATTCATACCTTACCTGCTGCTGCTGC	330
Qy	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
Db	331	TGTTTCTCCCTTCAAGACATATTTTGGCATCGTTCACACATGATGATGATGATGATG	390
Qy	81	TyrPanthrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	100
Db	391	TGGAATCTGAAATATGACACATGCTGCGATGATGGAACAGCCATGATGCGCCTGTG	450

QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
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QY 121 ValValLeuTrpAsnAlaGlnSerTyrTyrLeuTyrArgCysGlySerValLysAspGly 140
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QY 199 GlyLeuGln--PhePheArgLeuAlaSer-CysGly-GlnAspCysGlnValLysIleTr 217
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RESULT 8
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LOCUS 603035010F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176086 5'
DEFINITION mRNA sequence.
ACCESSION BI821143
VERSION BI821143.1 GI:15932693
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 792)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: sgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM1438 Row: 1 Column: 07
High quality sequence stop: 751.
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/clone_id="NIH_MGC_115"
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN
Alignment Scores:
Pred. No.: 2,27e-94 Length: 792
Score: 1031.50 Matches: 212
Percent Similarity: 92.21% Conservative: 1
Best Local Similarity: 91.77% Mismatches: 10
Query Match: 50.39% Indels: 9
DB: 4 Gaps: 1
US-10-077-111-13 (1-384) x BI821143 (1-792)

QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysGlnAlaPhe 20
|
|
|
Db 118 ATGGTGAATTAATGATTTCAACATTAAGCTGATCAAGAGATGATCAATGCTGCTTC 177
|
|
|
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
|
|
|
Db 178 TCCTTTCCCTCTGGCTACTGCTC--CTGGACAAACAAATTCGCTGATCTGTTACGT 234
|
|
|
QY 41 AspPheThrGlnLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysGly 60
|
|
|
Db 235 GACTTTTAACGAACTGGACACTGCTTCCATTGAAGATTTCATACCTATGCTGCTGCTGC 294
|
|
|
QY 61 CysPheSerProSerGlnHisIleLeuAlaSerCysSerThrAspGlyThrValLeu 80
|
|
|
Db 295 TGTTTCCCTCCCTCAGGACATAT-TTGGCATGCTGTTCAAACAGATGTTACCACTGTCTA 353
|
|
|
QY 81 TrpAsnThrGlnAsnGlyGlnMetLeuAlaValMetGlnGlnProSerGlySerProVal 100
|
|
|
Db 354 TGGAAATACGMAAATGAGACAGATGCTGGCAGTGAACAGCTTGTGGCACCCCTGTG 413
|
|
|
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlnValAlaAspGlyThr 120
|
|
|
Db 414 AGGGTTTGGCCAGTTTCCAGACTCCAGCTGTTGTCATCAAGGGGACCTGATGAACT 473
|
|
|
QY 121 ValValLeuTrpAsnAlaGlnSerTyrTyrLeuTyrArgCysGlySerValLysAspGly 140
|
|
|
Db 474 GTGGTTTGGGAAATGACAGTCAATCAAAATTAATGATGTGTGATGTTAAAGATGGC 533
|
|
|
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSer-Cy 160
|
|
|
Db 534 TCCTTGGCGGCAATGCAATTTCTCTTAATGAAGCTTCTTGTGCTGCTCTCAATG 593
|
|
|
QY 160 sGlyAspLeuThrValTyrAspAspLysMetArgCysLeuHisSerGln-LysAlaHisAs 180
|
|
|
Db 594 TGGTGAATTAACAGTGTGGATGATAAATGAGGTGTCTGCATATGAAATGAAGCTCATG 653
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|
|
QY 180 sPLeuGlyIleThr-CysCysAspPheSerSerGlnProValSer-AspGlyGlnGlnG 199
|
|
|
Db 654 ATCTTGAATTAACCTTGTGGCTGCGATTTTCTTTCACAGCAGTTTCTTGATGGAGAACAG 713
|
|
|
QY 199 YLeuGlnPhePheArg-LeuAlaSerCys-GlyGlnAspCysGlnValLys-IleTrpI 218
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|
|
Db 714 TCCTTCAAGTTTTCGCACTTGGCAATCATGTGGGTCAAGATTTGGCATGCAACATTTGGAC 773
|
|
|
QY 218 eValSerPheThrHisIle 224
|
|
|
Db 774 TGTTACTTTTACCATAATT 792
|
|
|

RESULT 9
CN793033 728 bp mRNA linear EST 26-MAY-2004
LOCUS CN793033
DEFINITION 4127990 BARC BBOV Bos taurus cDNA clone BBOV_46102 5', mRNA
sequence.
ACCESSION CN793033
VERSION CN793033.1 GI:47689013
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE	1 (pages 1 to 728)
AUTHORS	Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Metcunajall, L.K.
TITLE	Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL	Unpublished (2004)
COMMENT	Contact: Richard G. Baumann

FEATURES
SOURCE

Alignment Scores:	
Pred. No.:	1.0e-91
Score:	1005.00
Percent Similarity:	92.82%
Best Local Similarity:	87.08%
Query Match:	49.10%
8:	7
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	0

US-10-077-111-13 (1-384) X CN793033 (1-728)

Oy	MetValIysLeuIleHsTThrLeuAlaAspHsGlyAspAspValAsnCySAspAlaPhe	20
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Db	ATGTGTGAACATAATTCACACATTGACGATCATATATATATATGCAATCTGTGCTTTC	162
Oy	SerPheSerLeuLeuAlaThrCySerLeuAspIysThrIleArgLeuTyrSerLeuArg	40
:::.....	
Db	TCCCTCTTCCTCTTGGCTACTTGTGGCTTGAGCAAAACAATTGGCCATATTATTCCTGAGT	222
Oy	AspPheThrGluLeuProHsAspProLeuIysPheHisThrTyrIleValHisCySAsp	66
:::.....	
Db	GACTTTACCGAAGACATATCTCTCCATTGAAGTTTCACACCTATGCTGTCCACTGTGCTG	282
Oy	CysPheSerProSerGlyHisIleLeuAlaSerCySerThrAspGlyThrThrValLeu	80
:::.....	
Db	TGTTTTCCTCCCTTCAGACATATTATTTGGCTTCAATGTTCAACAAGATGGTACACATGTCCTCA	342
Oy	TyrAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	104
:::.....	
Db	TGGCATATCTCAAAACGGGACAGATTTTGGCAGCTAGATGGAACAGCCCACTGGTAACTCTGTG	404
Oy	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr	120
:::.....	
Db	AGAGTTTGGCCGATTTTCCCCAGACTTCACATGTTGTTGGCTTCAGAGGGGATCTCATGTGAAC	464

[illegible]

RESULT 10									
BO895162									
LOCUS	BO895162								
DEFINITION	BO895162	910 bp	mRNA	linear	EST 16-AUG-2000				
ACCESSION	AGENE000007.874888	NIH_MGC_130	Mus musculus	CDNA clone IMAGE:5334242					
VERSION	BO895162								
KEYWORDS	BO895162.1	GI:22287176							
SOURCE	EST.								
ORGANISM	Mus musculus	(house mouse)							
	Mus musculus								

REFERENCE	1 (bases 1 to 910)
AUTHORS	NIH-WGC http://wgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES

Location/Qualifiers

```

source
1. '910
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6334427"
/1ab_host="DH10B (phage-resistant)"
/clone_11b="N1H_MGC_130"
/notes="Organ: oocytes; Vector: pCMV-SPORT6.1; Site_1:
EcoRI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.95 kb. Constructed by
ResGen, Invitrogen Corp. Note: this is a N1H_MGC Library

```

Alignment Scores:	
Pred. No.:	1,46e-88
Score:	975.50
Percent Similarity:	88.89%
Best Local Similarity:	79.11%
Query Match:	47.66%
DB:	5
Length:	910
Matches:	178
Conservative:	22
Mismatches:	24
Indels:	1
Gaps:	1

US-10-077-111-13 (1-384) X BQ895162 (1-910)

QY 234 LysGlnPheThrGluAspTrpSerGluValValSerThrTrpLeuGlyAla 251
 Db 654 ---AAAGACACACTAAAGTGGGCACTGGCCCTGTTCT---TGGCCTTGCT 701

RESULT 12

CK306752 839 bp mRNA linear EST 01-MAR-2004
 SB02035A1D03.f1 normalized Keck-Tagu Library SB02 Taeniopygia
 guttata cDNA clone SB02035A1D03.f1 5, mRNA sequence.

ACCESSION CK306752
 VERSION CK306752.1 GI:44816326
 KEYWORDS EST.
 ORGANISM Taeniopygia guttata
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
 Estrilidae; Taeniopygia.
 1 (bases 1 to 839)
 Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
 Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
 and Liu,L.
 The Songbird Neurogenomics Initiative: An Evolving Public Resource
 for Study of Genes, Brain, and Behavior
 Unpublished (2004)
 Contact: David F. Clayton
 University of Illinois
 B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
 Tel.: 217 244 3668
 Fax: 217 244 1648
 Email: dclayton@uiuc.edu
 Base Calling/Quality Scores: PHRED from Washington University
 Genome Center.
 Vector Trimming: Cross match from Washington University Genome
 Center PHRAP suite. Low quality bases (Phred score < 20) were
 trimmed from both ends of the sequence by an in-house script.
 This sequence is vector free and at least 200 bp in length. Funded
 by PHS grant # R01 NS045264, 'Songbird Neurogenomics Initiative.'
 PCR Primers
 FORWARD: TAAATGACGACTGACTAGG(T7)
 BACKWARD: ATTAACCTCCTCAAG(T7)
 Insert Length: 839 Std Error: 0.00
 Plate: SB02035A1 row: D column: 03
 Seq primer: TAAATGACGACTGACTAGG (T7)
 High quality sequence stop: 839.

FEATURES

Source location/Qualifiers

1..839

/organism="Taeniopygia guttata"
 /mol_type="mRNA"
 /db_xref="taxon:59729"
 /clone="SB02035A1D03.f1"
 /rname_type="brain"
 /dev_stage="late embryo, post-hatch days 1, 10, 20, 45,
 and adult (pooled)"
 /lab_host="DH10B"
 /clone_lib="normalized Keck-Tagu Library SB02"
 /note="Organ: brain; Vector: pBS II SK(+); Site 1:
 EcoRI(5' side of insert); Site 2: NotI (3' side of
 insert); The library was constructed and normalized as
 described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
 (1996), Genome Research 6(9): 791-806. An identifying tag
 was added at the 3' during cDNA synthesis:
 insertAAAAAAAAAAAAAAAAATGCA."

ORIGIN

Alignment Scores:

Pred. No.: 1.24e-81 Length: 839
 Score: 907.00 Matches: 161
 Percent Similarity: 84.00% Conservative: 28
 Best Local Similarity: 71.56% Mismatches: 36
 Query Match: 44.31% Gaps: 0
 DB: 7

US-10-077-111-13 (1-384) x CK306752 (1-839)

QY 1 MetVallysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysGlyAlaPhe 20
 Db 90 ATGGCGACATTAAATTCACACTTATAGCAGATCATATGATGATTAATTACTGATGCTTC 149

QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspValThrIleArgLeuTyrSerLeuArg 40
 Db 150 TCATCTTGCTGCTTGGCTGACATGTTCTCTGGACAAACAAATTCGGCTATTTCTTGAGC 209

QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysGly 60
 Db 210 AACTTCGCTGAGCTCCCTACTCTCCGCTTGAGGCTCAGCGTACCGCTGACATGCTGC 269

QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu 80
 Db 270 TGTCTTCTGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 329

QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
 Db 330 TGGAGACACCCGCGATGGCGGCGAGGCTGCTGCTGAGACAGCCCGGCGCAGCTGCTC 389

QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
 Db 390 AGGCTCTGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449

QY 121 ValValLeuThrPheAlaGlnSerTyrIleLeuTyrArgCysGlySerValIleAspGly 140
 Db 450 GTGGTCTCTGGAACGTGACATGATGATGATGATGATGATGATGATGATGATGATGATG 509

QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
 Db 510 TCTTTGATGGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569

QY 161 GlyAspLeuThrValTTPAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
 Db 570 GGTATTTAAACATTTGGAGATGATTAATGATGATGATGATGATGATGATGATGATGATG 629

QY 181 LeuGlyIleThrCysGAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
 Db 630 CTGGCGCTTACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 689

QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValIleTyrPheValSer 220
 Db 690 AAATACCTCCAGATGGCTTCTGAGACAAATATCATCAAACTGCTATTTTG 749

QY 221 PheThrHisIleLeu 225
 Db 750 TTTCAGATTTCTTA 764

RESULT 13

CK792250 808 bp mRNA linear EST 25-FEB-2004
 LOCUS AGENCOURT.18674252 NIH MGC 230 Mus musculus cDNA clone
 DEFINITION IMAGE:30845589 5', mRNA sequence.

ACCESSION CK792250
 VERSION CK792250.1 GI:42804246
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/.
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@bds-remail.nih.gov
 Tissue Procurement: Shoko Kimura/Atsushi Yamada, (NCI,CCR)
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 25, 2005, 03:22:31 ; Search time 715 Seconds

(without alignments)
4432.164 Million cell updates/sec

Title: US-10-077-111-13

Perfect score: 2047
Sequence: 1 MWKLHTLADHDGDDVNCACF.....LTPNRLTKVAINRWLETHOK 384

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9772363 seqs, 4126298632 residues

Total number of hits satisfying chosen parameters: 19544726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO.spool/US10077111/runat_24102005_072848_8283/app.query.fasta_1.583
-DB=Published Applications NA -QPMT=fastlap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blowm62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTWT=pct -NORM=ext -HAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10077111@cgn 1 1 354 @runat_24102005_072848_8283
-NCPU=6 -ICPU=3 -NO MAP -LARGECQUERY -NEG SCORES=0 -WAIT -DSBBLCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCR_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq2:*
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22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US11A_NEW_PUB.seq:*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2047	100.0	1272	14 US-10-077-111-12	Sequence 12, Appl
2	1984	96.9	1553	14 US-10-077-111-3	Sequence 3, Appl1
3	1984	96.9	1818	14 US-10-077-111-1	Sequence 1, Appl1
4	1984	96.9	1996	21 US-10-357-930-23179	Sequence 23179, A
5	1984	96.9	1996	21 US-10-357-930-22046	Sequence 22046, A
6	1978	96.6	1773	17 US-10-287-218-40	Sequence 40, Appl1
7	1978	96.6	1773	20 US-10-474-291-40	Sequence 40, Appl1
8	1978	96.6	1811	18 US-10-104-047-1689	Sequence 1689, Ap
9	1978	96.6	1817	10 US-09-971-392-207	Sequence 207, App
10	1978	96.6	1844	16 US-10-037-270-768	Sequence 768, App
11	1978	96.6	1844	18 US-10-117-722-768	Sequence 768, App
12	1977	96.6	1821	22 US-10-956-157-5128	Sequence 5128, Ap
13	1958	95.7	1908	14 US-10-077-111-14	Sequence 14, Appl
14	1616.5	79.0	1901	14 US-10-077-111-6	Sequence 6, Appl1
15	1489	72.7	1400	22 US-10-956-157-10363	Sequence 10363, A
16	709	34.6	630	14 US-10-077-111-5	Sequence 5, Appl1
17	627.5	30.7	446	21 US-10-357-930-5029	Sequence 5029, Ap
18	626.5	30.6	409	21 US-10-357-930-14198	Sequence 14198, A
19	621.5	30.4	441	21 US-10-357-930-35319	Sequence 35319, A
20	621.5	30.4	441	21 US-10-357-930-44154	Sequence 44154, A
21	597	29.2	366	9 US-09-864-761-10657	Sequence 10657, A
22	532	26.0	297	9 US-09-864-761-27306	Sequence 27306, A
23	509	24.9	419	24 US-10-779-543-8962	Sequence 8962, Ap
24	352	17.2	520	14 US-10-077-111-8	Sequence 8, Appl1
25	318	15.5	399	24 US-10-779-543-12137	Sequence 12137, A
26	308.5	15.1	466	9 US-09-864-761-11052	Sequence 11052, A
27	300	14.7	180	9 US-09-864-761-27687	Sequence 27687, A
28	264.5	12.9	837	18 US-10-369-493-43585	Sequence 43585, A
29	264	12.9	3015	18 US-10-369-493-43929	Sequence 43929, A
30	263.5	12.9	1593	18 US-10-369-493-36600	Sequence 36600, A
31	261.5	12.7	1631	22 US-10-764-420-2108	Sequence 2108, Ap
32	259.5	12.7	3082	9 US-09-764-853-29	Sequence 29, Appl
33	259	12.7	3082	19 US-10-451-207-18	Sequence 18, Appl
34	256.5	12.5	3166	19 US-10-451-207-13	Sequence 13, Appl
35	251	12.3	1137	18 US-10-369-493-31840	Sequence 31840, A
36	250	12.2	1741	18 US-10-369-493-42880	Sequence 42880, A
37	246.5	12.0	1830	18 US-10-369-493-43872	Sequence 43872, A
38	245	12.0	840	18 US-10-369-493-43586	Sequence 43586, A
39	244.5	11.9	3420	18 US-10-369-493-42740	Sequence 42740, A
40	242.5	11.8	1965	18 US-10-369-493-43753	Sequence 43753, A
41	242.5	11.8	3408	18 US-10-369-493-42733	Sequence 42733, A
42	236.5	11.6	3358	18 US-10-369-493-42532	Sequence 42532, A
43	234.5	11.5	2826	26 US-11-097-143-17132	Sequence 17132, A
44	234.5	11.5	3965	26 US-11-097-143-14728	Sequence 14728, A
45	234.5	11.5	4826	26 US-11-097-143-17131	Sequence 17131, A

ALIGNMENTS

RESULT 1
US-10-077-111-12
; Sequence 12, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Todderud, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: JBA
; FILE REFERENCE: 3053-411US2
; CURRENT APPLICATION NUMBER: US/10/077, 111
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294, 181
; PRIOR FILING DATE: 2001-05-29

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/ PRIOR APPLICATION NUMBER: 60/269,366
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1272
/ LENGTH: 1272
/ TYPE: DNA
/ ORGANISM: HUMAN
/ FEATURE:
/ OTHER INFORMATION: RET 16.2 splice variant
US-10-077-111-12

Alignment Scores:
Pred. No.: 6,61e-233 Length: 1272
Score: 2047.00 Matches: 384
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-077-111-13 (1-384) x US-10-077-111-12 (1-1272)

QY 1 MetVallyLeuLeuLehIsthrLeuAlaAspHisGlyAspAspValAancCysCysAlaPhe 20
Db 111 ATGCTGAACCTGATTCACACATTAGCATGATCATGTCACATGTCACATGCTGCTTC 170
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrsSerLeuArg 40
Db 171 TCCCTTTCCCTCTGGCTACTGCTGCTTGGACAAACAAATCCGCTGACTGTTACGT 230
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyraAlaValHisCysCys 60
Db 231 GACTTTACTACACTGACACATTCCTCCATGAAGTTTCATCACTGCTGCTGCTGCTGC 230
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 291 TGTTCCTCCCTTCAGACATATTTTGGCATCGGTTCACAGATGGTACCACTGCTCTA 350
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 351 TGGAAATCTGAAAATGACAGATGCTGCGATGATGAAACAGCTTACTGCGACGCCCTGTG 410
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
Db 411 AGGCTTTGCCAGATTTCCACAGACTCCACGTGTTGGCATCAGGGCGACGCTGATGAACT 470
QY 121 ValValLeuThrPheAsnIleAsnSerTyrlsLeuTyrlsGlySerValLysAspGly 140
Db 471 GTGGTTTGTGGAAATGACAGTCACTACAAATATATATGATGTGTATGTTAAAGATGCG 530
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db 531 TCCCTTGGCGGCAATGTGATTTTCTCTTAATGAAAGCTTCTTTGTCACCTGCTCTCATGT 590
QY 161 GlyAspLeuThrValITrpAspAspLysMetArgCysLeuHisSerGlyLysValHisAsp 180
Db 591 GGTGATTTTACAGGTGTGGATGATATAAATGAGGTGTGTCATGTCGATAAAGACATGAT 650
QY 181 LeuGlyTleThrCysCysAspPheSerSerGlnProAlaSerAspGlyGluGlnGlyLeu 200
Db 651 CTGGAAATTAACCTGCTGCGATTTTCTTTCACAGCACTTTCTGATGGAGAAACAAGGCTTT 710
QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTPrIleValSer 220
Db 711 CAGTTTTTTTGGACGCGCATCATGTGCTCAGSATTGCCAATGCAAAATTTGGATTGTTCT 770
QY 221 PheThrHisIleLeuAlaArgArgThrGluHisGlnLeuLysGlnPheThrGluAspTrp 240
Db 771 TTATACCATATCTTATGACAGCGCAGCAATCATCAGCTGAAGCAATTTACCGAAGATTGG 830
QY 241 SerGluGluValAlaSerThrTrpLeuCysAlaGlnAspLeuLysAspLeuValGlyIle 260
Db 831 TCAGAGAGAGGTGCTCAACATGCTTTGTGCACAAATTTAAAGATCTTGTGTGATTT 890
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QY 261 PheLysMetAspAsnIleAspGlyLysGluLeuLeuAsnLeuThrLysGlnSerLeuAla 280
Db 891 TTCAGATGAAATTAACCTTGAATGGAAGAAAGAACTTTGAATCTTACAAAGAAAGCTTCGCT 950
QY 281 AspAspLeuLysIleGlnSerLeuGlyLeuArgSerLysValLeuArgLysIleGlnGlu 300
Db 951 GATGATTTGAAAATTTGAATCTCTAGACCTCGTAGTAAGTCTGAGAAAATTTGAAGAG 1010
QY 301 LeuArgThrLysValLysSerLeuSerSerGlyIleProAspGluPheIleCysProIle 320
Db 1011 CTCAGAGACCAAGGTAAATCCCTTCTTCAGAAATTCGATGAATTTATATGTCCAATA 1070
QY 321 ThrArgGluLeuMetCysAspProValIleAlaSerAspGlyTyrsSerTyrgLysGlu 340
Db 1071 ACTAGGAACCTTTATGAAGAATCCGCTCATCGCATCAGATGCGTATTCATATGAAAAGAA 1130
QY 341 AlMetGluAsnTrpIleSerLysLysArgThrSerProMetThrAnLeuValLeu 360
Db 1131 GCAATGGAATAATTGATTCAGCAAAAAGAAACGTACAAAGTCCCATGACAAATCTTGTCTT 1190
QY 361 ProSerAlaValLeuThrProAsnArgThrLeuLysMetAlaIleAsnArgTrpLeuGlu 380
Db 1191 CTTTCAGCGGTACTTACACCAATAGACTGTGAATAATGCGCATCAATGATGCTGGAG 1250
QY 381 ThrHisGlnLys 384
Db 1251 ACACACCAAAAG 1262

RESULT 2
US-10-077-111-3
/ Sequence 3, Application US/10077111
/ Publication No. US20020187492A1
/ GENERAL INFORMATION:
/ APPLICANT: Todderud, C. Gordon
/ APPLICANT: Finger, Joshua N.
/ APPLICANT: Rillema, Jili
/ TITLE OF INVENTION: TBA
/ FILE REFERENCE: 3053-4114US2
/ CURRENT APPLICATION NUMBER: US/10/077,111
/ PRIOR FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: 60/294,181
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 60/269,366
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 1553
/ TYPE: DNA
/ ORGANISM: HUMAN
US-10-077-111-3

Alignment Scores:
Pred. No.: 2.93e-225 Length: 1553
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 96.92% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 14 Gaps: 1

US-10-077-111-13 (1-384) x US-10-077-111-3 (1-1553)

QY 1 MetVallyLeuLeuLehIsthrLeuAlaAspHisGlyAspAspValAancCysCysAlaPhe 20
Db 111 ATGCTGAACCTGATTCACACATTAGCATGATCATGTCACATGTCACATGCTGCTTC 170
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrsSerLeuArg 40
Db 171 TCCCTTTCCCTCTGGCTACTGCTGCTTGGACAAACAAATTCGCTGACTGTTACGT 230
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyraAlaValHisCysCys 60
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Db 231 GACCTTACTGAACTGCACATCTTCATGAAAGTTTCATAGCTGTCACCTGCTGC 290
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu 80
Db 291 TGTTCCTCCCTTCAGAGCATATTTGGCATCGGTTCACAGATGGTACACAGCTCTTA 350
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 351 TGGAAATACATAAAATGGACAGATCTCGCATGATGAGAACAGCTTAGTGACGCCCTGTG 410
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAspGlyThr 120
Db 411 AGGCTTGGCCAGTTTCCAGACTCCACGTTGTGGCATCAGGGGAGCTGATGAACT 470
Qy 121 ValValLeuThrPheAlaGlnSerThrLysLeuThrArgCysGlySerValValAspGly 140
Db 471 GTGGTTTGGGAATGACAGCTCATCAAAATATATGAAATGTGTACTGTTAAAGATGC 530
Qy 141 SerLeuAlaAlaCysValPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db 531 TCCTTGGCGGATGTGATTTTCTCTTAATGAAAGCTTTCTTGTCACTGGCTCTCATGT 590
Qy 161 GlyAspLeuThrValThrPaspAspLysMetArgCysLeuHisSerGlyValAlaHisAsp 180
Db 591 GGTGATTTAACAGTGTGGATGATAAATGAGGTGTCTGCATAGTAAAGACATGAT 650
Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 651 CTGGGAATTAACCTGCTCGATTTTCTTTCACAGCAATTTCTGATGAGAACAGAGCTTT 710
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlyAspCysGlnValLysIleThrIleValSer 220
Db 711 CAGTTTTCGACCTGGCATGTGATGATGATGATGATGATGATGATGATGATGATGAT 770
Qy 221 PheThrHisIleLeu----- 225
Db 771 TTAAACCATATCTTAAGTTTGAATTAATAATATAAGTACATGAGTGGACATGTGCT 830
Qy 225 ----- 225
Db 831 CTTGTTCTGGCTGTGCTTTTCCCGTATGGGAGATGCTAGTCAAGGTCAGTGAAT 890
Qy 225 ----- 225
Db 891 AAGTCTGTCAATAGTATGATATGATTAATGAGATATGATCTTCAACATTTGACTCAGAC 950
Qy 225 ----- 225
Db 951 ACCAGTATGTCACACATGTGTGTTTGCACCTAATACCTTTTACTTGTACTGTTCA 1010
Qy 226 -----AlaArgArg 228
Db 1011 ATGACAAACAGTGAACATCTGCAATTTGACCTGGAACACTTTGCCAAGCAAGCGC 1070
Qy 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGlyGluValIleSerThrTrp 248
Db 1071 ACAGAACATCACTGAGACCAATTTACCGAATTTGGTCAAGAGATGTCTCAACATGG 1130
Qy 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
Db 1131 CTTTGTGCACAAAGATTTAAAGATCTTGTGTATTTTCAAGATGAATTAACATTGATGGA 1190
Qy 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuValIleGluSerLeu 288
Db 1191 AAAAACCTGTGAATCTTAAAGAAAGAGTGTGCTGATGATTTGAAATTTGAATCTCTA 1250
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuAlaGlyThrLysValLysSerLeu 308
Db 1251 GGACTGCTAGTAAGTCTCAGAGAAATTTCAAGAGCTCAGAGACCAAGTTAAATCCCTT 1310
Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db 1311 TCTTCAGGAATTCCTGATGAATTTATATGTCATTAATACAGAACTTAATGAAGATCCG 1370

Qy 329 ValIleAlaSerAspGlyTrpSerThrGluLysGluAlaMetGluAsnTrpIleSerLys 348
Db 1371 GTCAATGCATCAGATGAGTCTTTCATATGAAAGAAAGCAATGAAATTGATCAGCACA 1430
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1431 AAGAAAGTACAGATGCCATTCATGACAAATCTTCTTCTTCCAGCGGATTAACACCAAT 1490
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
Db 1491 AGGACTCTGAAATGCGCATCAATAGATGCTGAGACACACCAAAAG 1538
RESULT 3
US-10-077-111-1
: Sequence 1, Application US/10077111
: Publication No. US20020187492A1
: GENERAL INFORMATION:
: APPLICANT: Toddend, C. Gordon
: APPLICANT: Finger, Joshua N.
: APPLICANT: Rillema, Jill
: TITLE OF INVENTION: TBA
: FILE REFERENCE: 3053-4114US2
: CURRENT APPLICATION NUMBER: US/10/077,111
: PENDING FILING DATE: 2002-02-15
: PRIOR APPLICATION NUMBER: 60/294,181
: PRIOR FILING DATE: 2001-05-29
: PRIOR APPLICATION NUMBER: 60/269,366
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1818
: TYPE: DNA
: ORGANISM: HUMAN
US-10-077-111-1
Alignment Scores:
Pred. No.: 3,76e-225 Length: 1818
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatch: 1
Query Match: 96.92% Indels: 92
DB: 14 Gaps: 1
US-10-077-111-13 (1-384) x US-10-077-111-1 (1-1818)
Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
Db 148 ATGTGAAACTGATTCACACATTAGCTGATCATGTCAGATGTCACATGCTGCTGCTTC 207
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTrpSerLeuArg 40
Db 208 TCCCTTTCCTCTGTGGCTACTTCTCTCTTGGACAAACAAATTCGCTGTACTGTTAGCT 267
Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTrpAlaValHisCysCys 60
Db 268 GACTTATCTAACTGACCAATTCCTCATTAAGTTTATACCTATGCTGTCCACTGCTGC 327
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu 80
Db 328 TGTTCCTCCCTTCAGGACATATTTTGGCATTCGTTGCAACAGATGATCACTGCTCTA 387
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 388 TGGAAATCTGAAATGACAGATGCTGGCAGTATGAGAACAGCTTAGTGACAGCCCTGTG 447
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAspGlyThr 120
Db 448 AGGCTTGGCCAGTTTCCAGACTCCACGTTTGTGCATCAGGGGAGCTGATGAACT 507
Qy 121 ValValLeuThrPheAlaGlnSerThrLysLeuThrArgCysGlySerValLysAspGly 140

Db 508 GTGGTTTGTGGAATGCACATCATCAAAATTATATAGATGTGTGTTAAAGATGC 567
QY 141 SerLeuAlaIaIaCysAlaPheSerProArgGlySerPheValThrGlySerSerCys 160
Db 568 TCCCTGGCGGAGATGATTTTCTCCAAAGAAAGCTTTGTGCACTGGCTCCTCATGT 627
QY 161 GlyAspLeuThrValTTPaAspArgCysLeuHisSerGlyValHisAsp 180
Db 628 GGTGATTTAAGATGATGATTAATAAGGTGTGATGTGATAAAGACATGAT 667
QY 181 LeuGlyIleThrCysCysAspPheSerSerGlyProValSerArgGlyGlnGlyLeu 200
Db 688 CTGGAAATTCCTGCGGATTTTCTTCAAGCCAGCTTCTGATGGAACAAGGCTT 747
QY 201 GluPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValIleTPIleValSer 220
Db 748 CAGTTTTTGCAGCTGGCATATGTCAGAGATTGCCAAGTCAAAATTGGATTGTTCT 807
QY 221 PheThrHisIleLeu 225
Db 808 TTAAACCATATCTTAGCTTTGAATTAAATATATAAGTACACTGAGTGGCACTGTCT 867
QY 225 225
Db 868 CCGTTCTGGCTTGCTGCTTTTCCCATGATGGCAGATGCTAGTCAGGGTCAGTGAT 927
QY 225 225
Db 928 AAGTCTGTCACTAGTATATGATTAATACTGAGAAATTACTTACACATTGACTCAGCAC 987
QY 225 225
Db 988 ACCAGATATGCACAACCTTGCTTTTGGACCTTAATACCTTTACTTGCTAGTGTCA 1047
QY 226 226
Db 1048 ATGGAACAAAACAGTGAACATCTGCAATTGACCTGGAACAACCTTGCCAAGAGCGC 1107
QY 229 ThrGluHisGlnLeuGlySerPheThrGluAspTrpSerGlyGlnValValSerThrTrp 248
Db 1108 ACGAAACATCACTGAGAACATTTACGAAAGATTGGTCAGAGAGAGATGCTCAACATGG 1167
QY 249 LeuCysAlaGlnAspLeuValGlyIlePheLeuMetAsnIleAspGly 268
Db 1168 CTTGTGTCACAAAGATTAAAAAGATCTTGCTGTGATTTTCAAGATGAATTAATTGATGA 1227
QY 269 LysGluLeuLeuLeuThrLysGlnSerLeuAlaAspLeuValIleGlnSerLeu 288
Db 1228 AAGAACTGTTGAATCTTACAAAAGAAAGTCTGGCTGATGATTTGAAATTCCTA 1287
QY 289 GlyLeuArgSerLysValLeuArgLysIleGlnLeuArgThrLysValLysSerLeu 308
Db 1288 GGACTGGCTAGTAAAGTCTGAGGAAATTTGAAAGCTCAGAGACCAAGTTAAATCCCTT 1347
QY 309 SerSerGlyIleProAspGlnPheIleCysProIleThrArgLysLeuMetLysAspPro 328
Db 1348 TCTTCAAGAAATTCCTGATGATTTATATATGTCATTACTAGAGAATTATGAAGAATCCG 1407
QY 329 ValIleAlaSerArgGlyIleSerGlyGlnLysGlnAlaMetGluAsnTPIleSerLys 348
Db 1408 GTATCGCATCAGATGGCTATTCATATGAAGAAGAACAAATGGAAATTTGGATCAGAA 1467
QY 349 LysLeuArgThrSerProMetThrAsnLeuValLeuProSerAlaValIleThrProAsn 368
Db 1468 AAGAAAGTTCAGAGTCCCATGACAAATCTTGTCTTCTTCAAGCGGTACTTACCACAAT 1527
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHisGlnLys 384
Db 1528 AGGACTCTGAATAATGCCATCAATAGATGGCTGAGACACACCAAAAG 1575

RESULT 4
US-10-357-930-23179
/, Sequence 23179, Application US/10357930

Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endesge, Wilson
APPLICANT: Nonahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION: IDENTIFICATION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23179
LENGTH: 1996
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 2, 3, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994,
LOCATION: 1995, 1996
OTHER INFORMATION: n = A, T, C or G
US-10-357-930-23179

Alignment Scores:
Pred. No.: 4,366-225 Length: 1996
Score: 1984.00 Matches: 363
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 21 Gaps: 1

US-10-077-111-13 (1-384) x US-10-357-930-23179 (1-1996)

QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
Db 16 ATGGTGAACCTGATTCACACATTAAGTATCATGTGAGAGATGTCAACTGCTGTGCTTC 75
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTrpSerLeuArg 40
Db 76 TCCCTTTCCTCTTGGCTCTGCTCTTGGACMAAACAAATTCGCTGTACTGTTACGT 135
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyraIleValHisCysCys 60
Db 136 GACTTAACTGAAGTCCACATTTCTCATTTGAAGTTTCAATCACTATGCTGTCTGCTGC 195
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 196 TGTTCCTCCCTTCAGAGCATATATTGGCATGCTGTGTTAAAGATGATGATCACTGTCTTA 255
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 256 TGGAAATCACTGAATAATGAGACAGATGCGCAGATGAGAAACAGCTAAGTGCAGCCCTG 315
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValIleAspGlyThr 120
Db 316 AGGCTTTCAGATTTTCCCAAGACTCCACATGCTGTTGGCATCAGAGGAGAGCTGATGAACT 375
QY 121 ValValLeuTrpAsnAlaGlnSerTyrlLysLeuTyraArgCysGlySerValLysAspGly 140

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Db 376 GTGGTTTGGAGATGACAGTCTATACAAATTATATGATGTGTACTGTTAAAGATGC 435
Qy 141 SerLeuAlaAlaCysAlaPheSerProArgIYSerPheValThrGlySerSerCys 160
Db 436 TCCCTGGCGGCGATGTGATTTTCCCTTAATGAAAGCTTCTTGTGCACGTGCTCTCATGT 495
Qy 161 G1YAspPheThrVal1TTPAspAspLeuMetArgCysLeuHisSerGlyValAlaHisAsp 180
Db 496 GGTGATTTAAACAGTGTGGATGATTAATGAGTGTCTGATGATGAAAAGACATGAT 555
Qy 181 LeuGly1LeThrCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
Db 556 CTGGGAATTAACCTGCTCGATTTTCTTCCACAGCAGATTCTGATGAGAAACAAGTCTT 615
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspGlnValValSer1LeuValSer 220
Db 616 CAGTTTTCGACGTGGCATGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 675
Qy 221 PheThrHisIleLeu----- 225
Db 676 TTTAACCATATCTTGGTTTGAATTAAATATATAAAAGTACACTGAGTGGGCTGTGCT 735
Qy 225 ----- 225
Db 736 CCGTTCTGGGTTGTGCTTTTCCCATGATGGGAGATGCTAGTCTGAGGTCAGTGAT 795
Qy 225 ----- 225
Db 796 AAGTCTCATAGTATATGATTAATACTGAGATATGATTAATTACACATGACTCAGCAC 855
Qy 225 ----- 225
Db 856 ACCAGGATGTACACACTGTGCTTTTGGACCTAATACCTTTTACTGCTACTGTTCA 915
Qy 226 ----- 226
Db 916 ATGCAAAACAGTGAACATCTGGCAATTGACCTGGAACACTTGGCAAGCAAGGCGC 975
Qy 229 ThrGlnHisGlnLeuValSerPheThrGlnAspTrpSerGlnValValSerThrTrp 248
Db 976 ACAGAAATCATGAGTGAAGCAATTTACCAAGATTTGTCAGAGAGATGTCCTCAACATGG 1035
Qy 249 LeuCysAlaGlnAspLeuValGlyIlePheLeuMetAspAsn1LeuAspGly 268
Db 1036 CTTGTGCACAGATTTTAAAGATCTGTGTGATTTTCAAGATGAATTAACATGATGGA 1095
Qy 269 LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu 288
Db 1096 AAAGAACTGTTGATCTTACAAAGAAAGTCTGCTGATGATTTGAAATTTGATCTCTA 1155
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGlnGlnLeuArgThrLysValLysSerLeu 308
Db 1156 GGAATCGGTGTAAGTGTGAGGAAATTAAGAGCTCAGAGCAAGGTTAAATCCCTT 1215
Qy 309 SerSerGlyIleProAspGlnPheIleCysProIleThrArgGlnLeuMetLysAspPro 328
Db 1216 TCTTCAGGAATTCCTGATGAAATTAATATGTCATTAAGTAAAGAACTTAAGTAAAGATCCG 1275
Qy 329 ValIleAlaSerAspGlyTrpSerTrpGlnLysGlnLysGlnLysGlnLysGlnLys 348
Db 1276 GTCTATCCCATCAGATGCTATTCATATCAAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1335
Qy 349 LysLysValArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1336 AAGAAAGCTACAAATCCCATCAAAATCTTGTCTTCTTCCAGCGGTACTTACACAAAT 1395
Qy 369 ArgThrLeuLysMetAlaIleAsnArgThrLeuGlnLysGlnLys 384
Db 1396 AGGACTCTGAATAATGGCCATCAATGATGCTGGAGACACCAAAAG 1443

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RESULT 5
US-10-357-930-29046

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: Sequence 29046, Application US/10357930
: Publication No. US20040259086A1
: GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Endege, Wilson
: APPLICANT: Monahan, John
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
: TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
: TITLE OF INVENTION: HUMAN PROSTATE CANCER
: FILE REFERENCE: MRI-007BCN
: CURRENT APPLICATION NUMBER: US/10/357,930
: CURRENT FILING DATE: 2003-02-04
: PRIOR APPLICATION NUMBER: 09/785,276
: PRIOR FILING DATE: 2003-02-16
: PRIOR APPLICATION NUMBER: 60/183,119
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: 60/189,862
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: 60/207,454
: PRIOR FILING DATE: 2000-05-25
: PRIOR APPLICATION NUMBER: 60/211,314
: PRIOR FILING DATE: 2000-06-09
: PRIOR APPLICATION NUMBER: 60/219,007
: PRIOR FILING DATE: 2000-07-18
: PRIOR APPLICATION NUMBER: 60/255,281
: PRIOR FILING DATE: 2000-12-13
: NUMBER OF SEQ ID NOS: 62232
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 29046
: LENGTH: 1996
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1, 2, 3, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994,
: OTHER INFORMATION: n = A,T,C or G
US-10-357-930-29046

Alignment Scores:
Pred. No.: 4,36e-225 Length: 1996
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 21 Gaps: 1

US-10-077-111-13 (1-384) x US-10-357-930-29046 (1-1996)
Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
Db 16 ATGTGAAAGCTGATTCACATTAAGTATGATGATGATGATGATGATGATGATGATGATGAT 75
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTrpSerLeuArg 40
Db 76 TCCCTTTCCCTCTTGGTACTTGTCTCTTGGACAAACATTTGCCCTGACTGTTACGT 135
Qy 76 TCCCTTTCCCTCTTGGTACTTGTCTCTTGGACAAACATTTGCCCTGACTGTTACGT 135
Db 41 AspPheThrGlnLeuProHisSerProLeuLysPheHisThrTrpAlaValHisCysCys 60
Qy 41 AspPheThrGlnLeuProHisSerProLeuLysPheHisThrTrpAlaValHisCysCys 60
Db 136 GACTTTCTAAGCAAGCCACATTTCTCCATTAAGATTTATCTATGCTGTCCACTGCTGC 195
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 196 TGTTCCTCCCTTCAGGACATATTTTGGCATTCGTTGTCACAGATGGTACCACTGTCTTA 255
Qy 81 TrpAsnThrGlnAsnGlyGlnMetLeuAlaValMetGlnGlnProSerGlySerProVal 100
Db 256 TGGATATCTGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 315
Qy 101 ArgValLysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
Db 316 AGGGTTTGCAGATTTTCCCAAGACTCCACGATGTTTGGCATTCAGGGGACGCTGATGAAC 375

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QY 121 ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
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Db 376 GTGGTTTGGGATGCACAGTCAATACAAATTATATGATGTGTTATGTTAAAGATGCC 435
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPheValThrGlySerSerCys 160
| | | | |
Db 436 TCCTTGGCGGCATGTGCATTTTCCCTTAATGGAAGCTTCTTTTGCACGTGCTCTCATGT 495
QY 161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
| | | | |
Db 496 GGTGATTTACAGTGGGATGATTAATGAGTGTCTGCAATGTGAAAAAGCACATGAT 555
QY 181 LeuGlyLLeuTyrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
| | | | |
Db 556 CTGGAAATTAAGTCTGCTCGATTTTCTTCAACGCCATTTCTGATGGAACAAGCTCTT 615
QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpLLeuAlaSer 220
| | | | |
Db 616 CAGTTTCTTGGCAGTGCATGTGATGTGTCAGAGATTCGCAAAATTTGGATTTGTTCT 675
QY 221 PheThrHisIleLeu----- 225
| | | | |
Db 676 TTTTACCATATCTTAGTGTGTTGAATTAATAATTAAGTACACTGAGTGGGCACTGTCT 735
QY 225 ----- 225
| | | | |
Db 736 CTTGTTCTGGCTTGCTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGAGTCAAGTGA 795
QY 225 ----- 225
| | | | |
Db 796 AAGTCTGTCAATAGTATATGATTAATACTGAGAATATACTTCAACATTGACTCAGCAC 855
QY 225 ----- 225
| | | | |
Db 856 ACCAGGATATGCACAACCTTGTCTTTCACCTTAATACCTTTTACTTGGTACTGCTTCA 915
QY 226 -----AlaArgArg 228
| | | | |
Db 916 ATGAGCAAAACAGTGAACATCTGGCAATTTGACCTGGAAACATTTGCCAAGAGCGCG 975
QY 229 ThrGlnHisGlnLeuLysGlnPheThrGlnAspTrpSerGluGluValValSerThrTrp 248
| | | | |
Db 976 ACAGAACATAGCTGAAGCAATTTACGAAAGATTGGCAAGAGGAGATGCTCAACATCG 1035
QY 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyLLeuPheLysMetAsnAsnIleAspGly 268
| | | | |
Db 1036 CTTTGTGCACAAGATTTAAAGATCTTGTGTGATTTTCAAGATGAATTAACATTGATGGA 1095
QY 269 LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu 288
| | | | |
Db 1096 AAAGAACTGTGATCTTACAAAGAAAGTCTGGCTGATGATTTGAAATTTGATCTCTTA 1155
QY 289 GlyLeuArgSerLysValLysArgLysIleGlnGlnLeuArgThrLysValLysSerLeu 308
| | | | |
Db 1156 GGAAGTGGTGAAGTGAAGTGAAGAAATGGAAGAGTCAAGACCAAGGTAAATCCCTT 1215
QY 309 SerSerGlyLLeuProAspGlnPheIleCysProIleThrArgGlnLeuMetLysAspPro 328
| | | | |
Db 1216 TCTTCAGGAATTCCTGATGATTTATATGTCCAAATACAGAACTTAAGAAAGATCCG 1275
QY 329 ValIleAlaSerAspGlyLysSerTyrGlnLysGlnAlaMetGlnAsnTrpLLeuSerLys 348
| | | | |
Db 1276 GTATGCGCATCAGATGCTATTCATATGAAAGCAATGGAATTTGATCAGACAAA 1335
QY 349 LysLysArgThrSerProMetCThrAsnLeuValLeuProSerAlaValLLeuThrProAsn 368
| | | | |
Db 1336 AAAGAAACGTACAAGTCCATGACAAATCTGTCTTCTTCAAGGGGATCTTACACCAAAAT 1395
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHisGlnLys 384
| | | | |
Db 1396 AGGACTCTGAAAAATGGCATCAATAGATGCTGGAAGCACACCAAAAG 1443
RESULT 6

US-10-287-218-40
; Sequence 40. Application US/10287218
; Publication No. US20030198975A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.
; APPLICANT: BATRA, Sajeew; BAUGHN, Mariah R.
; APPLICANT: BECHA, Shanya D.; BOROMSKY, Mark L.
; APPLICANT: BUFORD, Neil; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
; APPLICANT: GANDHI, Ameena R.; GLEZEN, Kimberly J.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: HONCHELL, Cynthia D.; LAL, Preeti G.
; APPLICANT: LEE, Soo Yeun; LU, Dyoung Aina M.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: REDDY, Roopa; SANJANMALA, Madhu, M.
; APPLICANT: TANG, Y. Tom; WALIA, Nandinder K.
; APPLICANT: WANG, Yu-mei, E.; WARREN, Bridget A.
; APPLICANT: XU, Yuming; YANG, Junming
; APPLICANT: YAO, Monique G.; YUE, Henry
; APPLICANT: ZEBARJADIAN, Vaganeh
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: FI-0417 USA
; CURRENT APPLICATION NUMBER: US/10/287,218
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/11152
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/349,705
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/295,263
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/295,340
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/293,727
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/291,846
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/291,662
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/287,228
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/286,820
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/283,294
; PRIOR FILING DATE: 2001-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030198975A1 7483131CB1
US-10-287-218-40
Alignment Scores:
Pred. No.: 1,88e-224 Length: 1773
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 17 Gaps: 1
US-10-077-111-13 (1-384) x US-10-287-218-40 (1-1773)
QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
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Db 60 ATGCTAAACTGATTACACATTAGCTGATCATGTGACAGATGTCAATGCTGTGCTTTC 119
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
| | | | |

Db 120 TCCCTTTCCTCTGGCTACTGCTCTGACAAACAAATCGCTGCTACTGCTTACGT 179
Qy 41 AspPheThrGluLeuProHisSerProLeuIlePheHisThrValAlaHisCysCys 60:
Db 180 GACTTACTGAACGACGACATCTCCATTAAGTTTCACTAAGCTGCTGCTGCTGCTG 239
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 240 TGTCTTCCCTCCCTCAGGACATATTTTGGCATCGGTTCAACAGATGGTACACAGCTGCT 299
Qy 81 ThrAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 300 TGGAAATACGAAATAGCAGATGCTGCGAGTGTAGAACAGCCTAGTGGCAGCCCTGTG 359
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaIleAspGlyThr 120
Db 360 AGGGTTTGGCAGATTTTCCCGAGCTCCAGCTGTTGGCATCAGGGGAGCTGATGAGACT 419
Qy 121 ValValLeuThrAsnAlaGlnSerTyLeuLeuTyArgCysGlySerValIleAspGly 140
Db 420 GTGCTTTTGGGATGACAGCTCATCAATTAATATGATGTGCTACTGTTAAAGATGCG 479
Qy 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPheValIleThrGlySerSerCys 160
Db 480 TCCCTTGGCGGACATGTCATTTTCTCTTAATGAAAGCTTCTTGTCTGCTGCTCCTCATGT 539
Qy 161 GlyAspLeuThrValIleProAspAspLeuMetArgCysLeuHisSerGlyValAlaHisAsp 180
Db 540 GGGATTTTAAACAGTGGATGATGATTAATGAGGTGTGCTGATGTGAAAAAGCACATGAT 599
Qy 181 LeuGlyIleThrCysAspPheSerSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 600 CTGGATTAACCTGCTGCTGCTGCTTTTCTTCAACAGCACTTTCTGATGAGAAACAAGCTT 659
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValIleTyrIleValIleSer 220
Db 660 CAGTTTGTGACGCGCATGATGTGTGAGGATGCGCAAGCAAAATTTGGATTGTTCT 719
Qy 221 PheThrHisIleLeu----- 225
Db 720 TTTAACCATATCTTAAGTTTGAATTAATAATAAAAGTACACTGAGTGGGCACTGTGCT 779
Qy 225 ----- 225
Db 780 CCGTTTCTGGCTTGTGCTTTTCCCATGATGGGAGATGCTAGTCTCAGGCTCAGTGGAT 839
Qy 225 ----- 225
Db 840 AAGTGTCTCATATGATATGATTAATACTGAGATAATTAATTCTTCAACATTGACTCAGCAC 899
Qy 225 ----- 225
Db 900 ACCAGTATGTCAACACTTGTGCTTTTGCACCTTAATACCTTTTACTGCTACTGCTTCA 959
Qy 226 -----AlaArg 228
Db 960 ATGCACAAAACAGTGAACATCTGGCACTTGGAAACACTTTCGCAAGCAGAGAGAC 1019
Qy 229 ThrGluHisGlnLeuTyGlnPheThrGluAspTyrSerGlyGluValIleSerThrTyr 248
Db 1020 ACAGAAATCATGAGTGAAGCAATTTTACCGAAGATTTGTGAGAGAGAGATGTCTCAACATGG 1079
Qy 249 LeuCysAlaGlnAspLeuTyAspLeuValGlyIlePheLeuMetAsnIleAsnGly 268
Db 1080 CTTTGTGCACAAAGTTTAAAGATCTTGTGCTGTAATTTTCAAGATGAATTAACATTGATGGA 1139
Qy 269 LysGluLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuTySileGluSerLeu 288
Db 1140 AAAGAACTGTTGATCTTTACAAAGAAAGTCTGCTGATGATTTGAAATTTGATCTCTA 1199
Qy 289 GlyLeuAspSerLysValIleuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
Db 1200 GGAAGTGGTAAAGTGTGAGGAAAAATGMAAGCTCAGAGCAAGGTTAAATCCCTT 1259

Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db 1260 TCTTCAGGAATTCCTGATGATTAATTAATGCTCAATTAATGAGAACTTATGAAAGATCCG 1319
Qy 329 ValIleAlaSerAspGlyTyrSerTyGluLysGluAlaMetGluAsnTyrIleSerLys 348
Db 1320 GTCATGCGATCAGATGGCTATTCATATGAAGAAAGAACATGGAATTTGGATCAGCAAA 1379
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValIleThrProAsn 368
Db 1380 AAGAAAGTCAAGTCCCAAGACAAATCTTGTCTTCCCTCAGCGTACTTACACCAAAAT 1439
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTyrLeuGluThrHisGlnLys 384
Db 1440 AGAAGCTGCAAAATGGCCATCAATAGTGGCTGGAGACACACCAAAAG 1487
RESULT 7
US-10-474-291-40
Sequence 40: Application US/10474291
Publication No: US20040132043A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.
APPLICANT: BATRA, Sajeev; BAUGHN, Mariah R.
APPLICANT: BECHA, Shanya D.; BOROMSKY, Mark L.
APPLICANT: BURFORD, Vicki S.; EMERLING, Brooke M.
APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
APPLICANT: GRIFLIN, Jennifer A.; HARALIA, April J.A.
APPLICANT: HONCHELL, Cynthia D.; LAU, Preeti G.
APPLICANT: LEE, Soo Yeun; LU, Dying Aina M.
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.
APPLICANT: WANG, Y. Tom; CHAWLA, Nandinder K.
APPLICANT: WANG, Yu-Mei E.; WARREN, Bridget A.
APPLICANT: XU, Yuming; YANG, Junming
APPLICANT: YAO, Monique G.; YUE, Henry
APPLICANT: ZEBARJADIAN, Yeganeh
TITLE OR INVENTION: PROTEIN ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PI-0417 USN
CURRENT APPLICATION NUMBER: US/10/474,291
PRIOR FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: PCT/US02/11152
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/349,705
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/295,263
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/295,340
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/293,727
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/291,846
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/291,662
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/287,228
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/286,820
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/283,294
PRIOR FILING DATE: 2001-04-11
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 40
LENGTH: 1773
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: incycle ID No: 7483131CBI
US-10-474-291-40

Alignment Scores:

Pred. No.: 1,88e-224 Length: 1773
 Score: 1978.00 Matches: 382
 Percent Similarity: 80.25% Conservative: 0
 Best Local Similarity: 80.25% Mismatches: 2
 Query Match: 96.63% Indels: 92
 DB: 20 Gaps: 1

US-10-077-111-13 (1-384) x US-10-474-291-40 (1-1773)

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QY      1 MetValIyLeuIleHisThrLeuAlaAspHisGlyAspAspValAlaAspCysCysAlaPhe 20
DB      60 ATGGTAAACTGATTCACACATTAGCTGATCATGGATGACGATGTCAACTGCTGCTTC 119
QY      21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTySerLeuArg 40
DB      120 TCTTTTCCCTCTTGCTGCTACTGCTCTCTGGACAAACAAATGCGCTGTACTGTTACGT 179
QY      41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyAlaValHisCysCys 60
DB      180 GACTTACTGAACTGCGACATTTCTCCATTGAACTTTCATCTATGCTGCTCCACTGCTGC 239
QY      61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB      240 TGTTCCTCCCTTCAGGACATATTTTGGCATCTGTTCAACAGATGGTACCACTGCTCTA 239
QY      81 TrpAsnThrGluAsnGlyIleMetLeuAlaValMetGluGlnProSerGlySerProVal 100
DB      300 TGGAAATACGAAATAGACAGATGCTGGCAGTATGGAACAGACCTGATGGCAGCCCTGTC 359
QY      101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
DB      360 AGGCTTGGCCAGTTTCCCGACACTCCACCTGTTTGGCATCAGGGCAGCTGATGCAACT 419
QY      121 ValValLeuLeuTrpAsnAlaGlnSerTyrrLysLeuTyrrArgCysGlySerValLysAspGly 140
DB      420 GTGGTTTTGGCAATGCACAGTCATCAAAATTATATAGATGTGTAGTTAAAGATGTC 479
QY      141 SerLeuAlaAlaCysValaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
DB      480 TCTTTGGCGGCAAGTGATTTCTCTCTAATGAAGCTTCTTTGCACTGGCTCTCTCATGT 539
QY      161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
DB      540 GGTGATTTAACTGCTGGGATGATAAATGAGGTGCTGCATAGTGAAGAAACACATGAT 539
QY      181 LeuGlyIleThrCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
DB      600 CTGGGAATTCCTGCTGCGATTTTCTTTCACAGCCAGTTTCTGATGGAGAACAGGCTT 659
QY      201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer 220
DB      660 CAGTTTTCGACTGGCATCATGTGGTCAGGATTGGCCAAAGTCAAAATTGGATTGTTCT 719
QY      221 PheThrHisIleLeu----- 225
DB      720 TTTAACCATATCTTAGGTTTGAATTAATAATAAAGTACACTGAGTGGCACTGTGCT 719
QY      225 ----- 225
DB      780 CCTGTTCTGGCTTGTGCTTTTCCCATGATGGCAGATGCTACTTCAGGGTCAGTGGAT 839
QY      225 ----- 225
DB      840 AAGTCTGTCACTAGTATATGATTAATACTGAGAAATATACTTACACATTGACTCAGCAC 899
QY      225 ----- 225
DB      900 ACCAGTATGTCACAACTTGTGCTTTTGACACTAATACCTTTTACTTGCTACTGATCA 959
QY      226 -----AlaArgArg 228
  
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DB      960 ATGGACAAACAGTGAACATCTGGCAATTGACCTGAAAAACCTTGGCCACAGCAGAC 1019
QY      229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGlyGluValLysThrTrp 248
DB      1020 ACAGAACATCAGCTGGAAGCAATTTTACCGAAGATTGTCAGAGAGAGATGCTTCACATGG 1079
QY      249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
DB      1080 CTTTGTGCACAGATTTTAAAGATCTTGTGGTATTTTCAAGATGAATAACATGATGGA 1139
QY      269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
DB      1140 AAGAACTGTTGATTTTCAAAAGAAAGAACTGCGCTGAGATTTGAAATTGAAATCTTCA 1199
QY      289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
DB      1200 GGACTCGTAGTAAGTGTGAGGAAATTAAGAGCTCAGGACCAAGGTTAAATCTCTT 1259
QY      309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
DB      1260 TCTTCAGGAATTCCTGATGATTAATTAATGTCATGCAATGAGAACTTATGAAGAATCCG 1319
QY      329 ValIleAlaSerAspGlyTyrrSerTyrrGlyLysGluAlaMetGluAsnTrpIleSerLys 348
DB      1320 GTCATGCAATCAGATGCTAATTCATATGAAAGAAAGCAATGAAATTTGGATCACCAAA 1379
QY      349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerValAlaLeuThrProAsn 368
DB      1380 AAGAAACGTACAGATCCCATGACAAATCTTGTCTTCCCTTCAGGGTACTTACACCAAT 1439
QY      369 ArgThrLeuLysMetAlaIleAsnArgTyrrLeuGluThrHisGlnLys 384
DB      1440 AGGACTGTGAAATGGCCATCAATAGATGCTGGAGACACACCAAAAG 1487

RESULT 8
US-10-104-047-1689
; Sequence 1689, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1ol full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1689
; LENGTH: 1811
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1689

Alignment Scores:
Pred. No.: 1.94e-224      Length: 1811
Score: 1978.00      Matches: 382
Percent Similarity: 80.25%      Conservative: 0
Best Local Similarity: 80.25%      Mismatches: 2
Query Match: 96.63%      Indels: 92
DB: 18      Gaps: 1

US-10-077-111-13 (1-384) x US-10-104-047-1689 (1-1811)

QY      1 MetValIyLeuIleHisThrLeuAlaAspHisGlyAspAspValAlaAspCysCysAlaPhe 20
DB      150 ATGGTAAACTGATTCACACATTAGCTGATCATGGATGACGATGTCAACTGCTGCTTC 209
QY      21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTySerLeuArg 40
DB      210 TCTTTTCCCTCTTGCTGCTACTGCTCTCTGGACAAACAAATGCGCTGTACTGTTACGT 269
QY      41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrrAlaValHisCysCys 60
  
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Db 270 GACTTACTGACGACATTCCTCATGTGAAGTTTATACCTATGCTGCTCACTGCTGC 329
Qy 61 CyPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 330 TGTTCCTCCCTCCAGACATATTTTGGCATCGGTTCACAGATGGTACCACTGCTCTTA 389
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 390 TGGAAATCTGAATAATGACAGATGCTGGCATGTGGAACGCTTAAGTGGACGCTGTG 449
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
Db 450 AGGCTTTGCCAGTTTCCCGAGACTCCACGTTGTCATCAGGGGACAGCTGATGAACT 509
Qy 121 ValValLeuThrPheAsnAlaGlnSerThrLysLeuThrArgCysGlySerValLysAspGly 140
Db 510 GTGGTTTGTGGAATGACAGCTCATACAAATTATATGATGCTGATGTTAAAGATGCG 569
Qy 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db 570 TCCTTGGCGGATGTGATTTCTCTTAATGGAAGCTTCTTGCTGCTGCTCTCTCATGT 629
Qy 161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
Db 630 GGTGATTTAACAGTGTGGATGATAAATAGAGTGTCTGCACTAGTGAAGAACCATGAT 689
Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 690 CTGGAATTCACGCTGCGATTTTCTTTCACAGCCAGTTTCTGATGAGAAACAAGTCTT 749
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleThrPheValSer 220
Db 750 CAGTTTTCGACGTCGATCATGTGTCAGATGCCAAGTCAAAATTTGGATTGTTCT 809
Qy 221 PheThrHisIleLeu----- 225
Db 810 TTTAACCATATCTTAGCTTTTGAATTAAATATAAAAGTACAGTGGGCACTGTGCT 869
Qy 225 ----- 225
Db 870 CCTGTCTGCTGTGCTGCTTTTCCCATGATGGGAGATGCTAGTCTCAGGGTCAGTGAT 929
Qy 225 ----- 225
Db 930 AAGTCTGTCAATGATATGATACTAATACTGAGAATATCTTCAACATGACTCAGCAC 989
Qy 225 ----- 225
Db 990 ACCAGATATGACACACTTGTGCTTTGCACTAATACCTTTTACTTGTGCTACTGTTCA 1049
Qy 226 -----AlaArgArg 228
Db 1050 ATGACAAATAACAGTGAACATCTGGCAATTGACCTGGAACACTTGGCCAAAGAGAGC 1109
Qy 229 ThrGlnHisGlnLeuLysGlnPheThrGluAspTrpSerGlyGluValValSerThrTrp 248
Db 1110 ACAGAAATACATGCTGAAGCAATTTTACGAAGATTGGTCAGAGAGAGATGTCCTCAACATGG 1169
Qy 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetCAsnAsnIleAspGly 268
Db 1170 CTTTGTGTCACAAAGTTTAAAGATCTTGTGGTATTTTCAAGATGAATACATTGATGGA 1229
Qy 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuValLysIleGluSerLeu 288
Db 1230 AAAGAACTGTTGATCTTACAAAGAAAGTCTGGCTGATGATTTGAAATGATCTCTTA 1289
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
Db 1290 GGATTCGCGTAAAGTCTGAGAAATGAAAGCTCAGAGACCAAGGTTAAATCCCTT 1349
Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328

Db 1350 TCTTACGAATTCCTGATGATTAATATGTCCATAACTAGAGAACTTATGAAAGATCCG 1409
Qy 329 ValIleAlaSerAspGlyTrpSerThrGluLysGluAlaMetGluAsnThrPheSerLys 348
Db 1410 GTCATGCAATCAATGCTATTCATATGAAAGAACCAATGGAATTTGGATCAGCAA 1469
Qy 349 LysIleArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1470 AAGAAAGTACAACTCCCATGACAAATCTGTTCTTCTTCCAGGGTACTTACCCAAAT 1529
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
Db 1530 AGGACTCTGAATAATGGCCATCAATGATGCTGAGACACACCAAG 1577
RESULT 9
US-09-971-392-207
Sequence 207, Application US/09971392
Publication No. US20030134283A1
GENERAL INFORMATION:
APPLICANT: Peterson, David P.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
FILE REFERENCE: PA-0029 US
CURRENT APPLICATION NUMBER: US/09/971,392
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/237,652
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PERL Program
SEQ ID NO 207
LENGTH: 1817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Template ID: 158923.9
US-09-971-392-207
Alignment Scores:
Pred. No.: 1,95e-224 Length: 1817
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 10 Gaps: 1
US-10-077-111-13 (1-384) x US-09-971-392-207 (1-1817)
Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValaLysCysValaPhe 20
Db 148 ATGTGAAACTGATTCACACATTAAGTATGATGATGATGATGATGATGATGATGATG 207
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTrpSerLeuArg 40
Db 208 TCCCTTTCCCTCTTGGCTACTTGTCTTGGACAAAACAATTGGCCGTACTGCTTACGT 267
Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyralaValHisCysCys 60
Db 268 GACTTACTGAACTGCACATTTCTCCATGGAAGTTTCATACCTATCTGTCACACTGCTGC 327
Qy 61 CyPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 328 TGTTCCTCCCTCCAGACATATTTTGGCATCGGTTCACAGATGGTATGCCACTGTCTTA 387
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 388 TGGAAATCTGAATAATGACAGATGCTGGCATGTGGAACGCTTAAGTGGACGCTGTG 447
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
Db 448 AGGCTTGGCAGATTTTCCCGAGACTCCACGTTGTCATCAGGGGACAGCTGATGAACT 507

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QY 121 ValValLeuTrpAsnAlaGlnSerTyrLeuLeuTyrArgCysGlySerValIlyAspGly 140
DB 508 GGGGTTTGTGGAATGCACAGTCATCAAAATTATATAGATGTGTAGTTAAAGATGGC 567
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
DB 568 TCCCTGGCGGACGTCATTTCTCCAAAGAGCTCTTTGTCTCATGCTGCTCCTCATGT 627
QY 161 GlyAspLeuThrValTrpAspAspIlyMetArgCysLeuHisSerGlyIlyAspAlaHisAsp 180
DB 628 GGTGATTTAACTGCTGGGATGATTAATAAGGTGTCTGATAGTGAATAAGACATGAT 687
QY 181 LeuGlyIlyLeuThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
DB 688 CTGGGAATTACCTGCTGCGATTTTCTCTTCACAGCCAGTTTCTGATGGAGAACAAGGTCTT 747
QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValIlyIleThrPleValSer 220
DB 748 CAGTTTTTTCGACTGCGATCATGTGTGTCAGGATTTGCCAAATTCGAATTTGGATTTCTT 807
QY 221 PheThrHisIleLeu----- 225
DB 808 TTTAACCATATCTTAGGTTTGAATTAATAATATAAAAGTACACTGAGTGGGCACTGTGCT 867
QY 225 ----- 225
DB 868 CCTGTTCTGGCTTGTGCTTTTTCCTCATGATGGCAGATGCTAGTCTCAGGGTCAGTGAT 927
QY 225 ----- 225
DB 928 AAGTCTGTCTAGTATATGATACTAATACTGAGAATATACTTCAACATTGACTCAGCAC 987
QY 225 ----- 225
DB 988 ACCAGGTATGTCAACACTGTGCTTTTGCACCTAATACCTTTACTGTCTAGTGGTTCA 1047
QY 226 ----- 226
DB 1048 ATGAGCAAAACAGTGAACATCTGCAATTTGACCTGGAAACACTTGGCCAAAGAGAGC 1107
QY 229 ThrGlnHisGlnLeuIlyGlnPheThrGlnAspTrpSerGlnGlnValIlySerThrTrp 248
DB 1108 ACGAAACATCAGCTGAAGCAATTTACCGAAGATTGGTCAAGAGGAGATGCTCAACACTGG 1167
QY 249 LeuCysAlaGlnAspLeuIlyAspLeuValGlyIlyPheIlyMetAsnAlaIleAspGly 268
DB 1168 CTTGTGTGCACAAATTTAAAGATCTTGTGTGATTTTCAAGATGAATTAACATTGATGGA 1227
QY 269 IlyGlnIleLeuIlyAsnLeuThrIlyGlnSerLeuAlaAspAspLeuIlyGlnSerLeu 288
DB 1228 AAAAGAACTGTTGAATCTTACAAAGAAAGCTGCTGATGATTTGAAAATTTGAATCTCTA 1287
QY 289 GlyLeuAspSerIlyValLeuArgIlyIleGlnGlnLeuArgThrIlySerValIlySerLeu 308
DB 1288 GGACTGCTGATGAAGTCTGAGGAAATATGAAGAGTCAAGACCAAGGTTAAATCCCTT 1347
QY 309 SerSerGlyIlyLeuProAspGlnPheIleCysProIleThrArgIlyLeuMetIlyAspPro 328
DB 1348 TCTTTCAGGAATTTCTGATGAATTTATATATGTCAAATACTAGAGAACTTATGAAGATCCG 1407
QY 329 ValIleAlaSerArgGlyIlySerTyrGlnIlyGlnAlaMetGlnLeuThrIlySerIly 348
DB 1408 GTCATGCGATCAATGCTATTCATATGAAAAGAAAGCAATGAAAATTTGATCAGCAAA 1467
QY 349 IlyIlyAspArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1468 AAGAAACGATCAAGTCCCATGACAAATCTGTCTTCAAGGGACTTACCACAAT 1527
QY 369 ArgThrLeuIlyMetAlaIleAsnArgTrpLeuGlnThrHisGlnIly 384
DB 1528 AGGACTCTGAATAATGGCCATCAATAGATGCTGAGAGCACACCAAAAG 1575
RESULT 10
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US-10-037-270-768
; Sequence 768, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aseudi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Weinman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Dermanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: PC_FL_genes Version 1.0
; SEQ ID NO 768
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-037-270-768
Alignment Scores:
Pred. No.: 2e-224 Length: 1844
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 96.63% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 16 Gaps: 1
US-10-077-111-13 (1-384) x US-10-037-270-768 (1-1844)
QY 1 MetValIlyLeuIleHisThrLeuAlaAspHisGlyAspAspValAlaGlnCysCysAlaPhe 20
DB 164 ATGGTAAACCTGATTTATACACATTTAGCTGATCATGTGACGATGTCNACTGCTGCTTC 223
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspIlyThrIleArgIlyCutySerLeuArg 40
DB 224 TCTTTTCCCTCTTGCTGCTAGTCTGCTCTTGGACAAACAAATTCGCTGACTGTTAGCT 283
QY 41 AspPheThrGlnLeuProHisSerProLeuIlyPheHisThrTyrAlaValHisCysCys 60
DB 284 GACTTATCTGAACTGGCCACATTTCTCATTTGAAGTTTCATACCTATGCTGTCCACTGCTGC 343
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB 344 TGTTTCTCCCTTCAGACATATTTTGGCATGCTGTTCACACAGATGTACCACTGCTCTA 403
QY 81 TrpAsnThrGlnAsnGlyIlyMetLeuAlaValMetGlnGlnProSerGlySerProVal 100
DB 404 TGGAAATATCGAAAAATGACAGATGTGCGCAGTGAAGAACAGGCTGAGCCCTGTG 463
QY 101 ArgValCysGlnPheSerProAspSerThrCysIleLeuAlaSerGlyValAlaAspGlyThr 120
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Db 464 AGGTTTCCAGTTTCCAGACTCCAGCTGTTGGCATACAGGGCAGCTGATGAACT 523
Qy 121 ValValLeuThrPheAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
Db 524 GTGGTTTGGGAATGACAGATCATTAACAAATTATATGATGATGCTAGCTTTAAAGATGCG 583
Qy 141 SerLeuAlaIaCysAlaPheSerProAsnGlySerPheValThrGlySerSerCys 160
Db 584 TCCTTGGCGGACATGATTTCTCCCTAAATGGAAGCTCTTTGTCACCTGGCTCTCTACTGT 643
Qy 161 GlyAspLeuThrValTyrPheAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
Db 644 GGTGATTTAATCAGTGTGGATGATTAATGAGGTGCTGCATAGTGAATAAGACATGAT 703
Qy 181 LeuGlyTleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 704 CTGGGAATTAACCTGCGCGAATTTTCTTTCACAGCAATTTCTGATGGAACAAGGCTCTT 763
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTyrPileValSer 220
Db 764 CAGTTTTTTCAGCTGGCATGTGTCAGAGATTGCCAAGTCAAAATTTGATTTGTTCT 823
Qy 221 PheThrHisIleLeu----- 225
Db 824 TTTAACCATATCTTAGCTTTGAATTAATAATATAAAGTACACTGAGTGGGCACTGTGCT 883
Qy 225 ----- 225
Db 884 CTTGTTCTGGCTGTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGGCTCAGTGGAT 943
Qy 225 ----- 225
Db 944 AAGTCTGTCAATGATATGATACTAATACGAGAATATCTTCAACATTTGACTCAGCAC 1003
Qy 225 ----- 225
Db 1004 ACCAGTATGTCACAACTGTGTGTTTGGACCTAATACCTTTACTGTGACTGTTCA 1063
Qy 226 -----AlaArgArg 228
Db 1064 ATGGACAAACAGTGAAATCTGGCAATTGACCTGGAACACTTTGCCAAGCAAGAGGC 1123
Qy 229 ThrGlnHisGlnLeuLysGlnPheThrGlnAspTyrSerGluGluValIleValSerThrTyr 248
Db 1124 ACAGAAATCACTGCAAGCAATTTACCGAAGATTGGTCAAGAGGAGATGTCTCAACATGG 1183
Qy 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
Db 1184 CTTTGTGCACAAAGATTTAAAGATCTTGTGGTATTTTCAAGATGAATTAACATTGATGGA 1243
Qy 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
Db 1244 AAAGAACTGTTGATCTTACAAAGAAAGCTGGCTGATGATTTGAAATTTGAATCTCTA 1303
Qy 289 GlyLeuArgSerLysValLysArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
Db 1304 GGACTGCTAATAAGTCTGAGGAAATTTGAAGCTCAGAGCAACCAAGTTAAATCCCTT 1363
Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db 1364 TCTTCAGGAATCTCTGATGAATTTATATGTCCAATTAACAGAACTTATGAAGATCCG 1423
Qy 329 ValIleLeuSerAspGlyTyrSerTyrGluLysGluLysMetGluAsnTyrPileSerLys 348
Db 1424 GTCAATCCATCAGATGCTATTCATATGAAGAAAGAAAGCAATTTGATCAGCAAA 1483
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValIleLeuThrProAsn 368
Db 1484 AAGAAACGTACAAGTCCCATACCAATTTCTTCTTCAAGGCTACTTACACCAAT 1543
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTyrLeuGlnThrHisGlnLys 384
Db 1544 AGGACTCTGAATAATGGCCATATGATGCTGAGAGACACCAAAAG 1591

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RESULT 11
US-10-117-722-768
; Sequence 768, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Dumanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_fl_genes Version 1.0
; SEQ ID NO 768
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-117-722-768

Alignment Scores:
Pred. No.: 2e-224 Length: 1844
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best local Similarity: 96.63% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: Gaps: 1

US-10-077-111-13 (1-384) x US-10-117-722-768 (1-1844)
Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
Db 164 ATGGTGAACGTGATTCACACATTTAGCTGATCATGATGATGATGATGATGATGATGATG 223
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
Db 224 TCCCTTTCCCTCTGGCTACTGCTCTCTTGGACAAAACAATTCGCTGACTGCTTACGT 283
Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
Db 284 GACTTTACTGAACGCGCACATTCCTCAATTGAAGTTTATCATGCTATGCTGCTCACTGTC 343
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 344 TGTTTCTCCCTTCAGGACATATTTTGGCATTCGTTTCAACAGATGCTACACTGCTCTA 403
Qy 81 TrpAsnThrGlnAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 404 TGGAAATACGAAATGACAGATGCTGCAAGTGAAGACGCTTACTGACAGCCCTGTG 463
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaIleAspGlyThr 120
Db 464 AGGCTTTGCCAGATTTTCCAGACTCCACAGTGTGTCATCAGGCGCAGCTGATGAAC 523
Qy 121 ValValLeuThrPheAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
Db 524 GTGGTTTGGGAATGACAGTCTATTAACAAATTATATGATGATGCTAGCTTTAAAGATGCG 583
Qy 141 SerLeuAlaIaCysAlaPheSerProAsnGlySerPheValThrGlySerSerCys 160

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Db      584 TCCCTGGCGGCGATGTCATTTCTCCTAATGAGACCTTTTTCATGCTGCTCCATGT 643
QY      161 G|YAspLeuThrVal|TrpAspAspLysMetArgCysLeuHisSerGluValAsp 180
Db      644 GGGATTTTAACTGATGGGATGATAAATAGAGGTGCTGATGTGAAAAAGCACATGAT 703
QY      181 LeuGly|IleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlyLeu 200
Db      704 CTGGAAATTACCTGCTGCGATTTTCTTCTCAACGCAATTTCTGATGGAGAACAGGCTT 763
QY      201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValylIleTrpIleValSer 220
Db      764 CAGTTTTTTTGAGCTGCGATCATGTGTGACAGATTGCCAAGTCAAAATTTGATGTGTTCT 823
QY      221 PheThrHisIleLeu----- 225
Db      824 TTTTACCATATCTTATAGTTTGAATTAATAATATAAGTACACTGAGTGGCACTGTGCT 883
QY      225 ----- 225
Db      884 CCGTTCTGCGCTTGCTTTTCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGGAT 943
QY      225 ----- 225
Db      944 AAGCTGTCTAGTATATAGTACTAATACTAGAGATATACTTCAACATTGACTCAGCAC 1003
QY      225 ----- 225
Db      1004 ACCAGGATGTCAACACTTGTGCTTTTGCACTAATACCTTTTACTTGCTACTGCTCA 1063
QY      226 -----AlaArgArg 228
Db      1064 ATGAGCAAAACAGTGAACATCTGGCAATTGACCTGGAAACACTTTGCCAAGCAGAGAGC 1123
QY      229 ThrGlnHisGlnLeuLysGlnPheThrGlnAspTrpSerGluValValSerThrTrp 248
Db      1124 ACGAAACATCAGCTGAGCAATTTTACGGAAGATTGGTCAGAGAGGATGTGCTCAACATGG 1183
QY      249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
Db      1184 CTTTGTGCACAACTTTTAAAGATCTTGTGGTGTGTTTTCAGATGATTAACATTGATGGA 1243
QY      269 LysGluLeuLeuValLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
Db      1244 AAGAACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAAATTGAACTCTTA 1303
QY      289 GlyLeuAspSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
Db      1304 GGACTGCGTAGTAAGTGTGAGGAAAAATTGAAGAGCTCAGACCAAGGTTTAAATCCCTT 1363
QY      309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db      1364 TCTTCAGGAATTCCTGATGAATTTATATGTCCAATACAGAACTTATGAAGATCCG 1423
QY      329 ValIleAlaSerAspGlyIleLysSerIleGluLysGluAlaMetGluLeuTrpIleSerLys 348
Db      1424 GTCATGCGCATCAATGCGTATTCATATGAAGAAAGAGCAATGAGAAATTTGATCAGCAA 1483
QY      349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuTrpProAsn 368
Db      1484 AAGAAACGTAACAAGTCCCATGACAAATCTTGTCTTCCACGGGACTTAAACCAAAAT 1543
QY      369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
Db      1544 AGGACTCTGAATAATGGCCATCAATAGTGGCTGGAGACACCAAAAG 1591

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RESULT 12
US-10-956-157-5128

; Sequence 5128, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounst, William

```

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTASES;
; FILE REFERENCE: 031696-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5128
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5128

Alignment Scores:
Pred. No.: 2,576-224 Length: 1821
Score: 1977.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.58% Indels: 92
DB: Gaps: 1

US-10-077-111-13 (1-384) x US-10-956-157-5128 (1-1821)

QY      1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
Db      159 ATGCTGAACCTGATTCACACATTAGCTGATCATGTGACAGATGTCAACTGCTGCTTC 218
QY      21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTrpSerLeuArg 40
Db      219 TCCTTTCCCTCTTGCTGCTACTGCTCTCTTGAGAAAAACAATTTGCTGTACTCTTACGT 278
QY      41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyraIleValHisCysCys 60
Db      279 GACTTACTGAACTGGCACATTTCTCATTTGAAGTTTCAATACCTATCTGTCCACTGCTG 338
QY      61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db      339 TGTTCCTCCCTTCAGAGACATATTTGGCATCGTTTCAACAGATGCTACCACTGTCTTA 398
QY      81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db      399 TGGAAATACGAAATATGACAGATGCTGGCAGATGATGAACACGCTGTGTGCGACCCCTG 458
QY      101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
Db      459 AGCGTTTGCAGATTTTCCCAAGCTCCACGCTGTGTGCAATCAGGGGCAGCTGATGGA 518
QY      121 ValValLeuTrpAsnAlaGlnSerTyrlLysLeuTyraArgCysGlySerValLysAspGly 140
Db      519 GTGGTTTGTGGAATGCACAGTCATATCAAAATTATATAGATGTGTGTGTTAAAGATG 578
QY      141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPheProValThrGlySerSerCys 160
Db      579 TCCTTTGGCGCATGTCAATTTTCTCTAATGGAAGCTTCTTGTGCTGCTGCTCTCATATG 638
QY      161 GlyAspLeuThrVal|TrpAspAspLysMetArgCysLeuHisSerGlnValylIleTrpIleValSer 180
Db      639 GGTGATTTTAACTGATGGGATGATTAATAGAGGTGTCCCATAGTGAATAAAGCACATGAT 698
QY      181 LeuGly|IleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
Db      699 CTGGAAATTACCGTGGCATTTTCTTCTCACAGCCAGTTTTCATGATGAGAACACAAAGGCTCTT 758
QY      201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValylIleTrpIleValSer 220
Db      759 CAGTTTTTTTGAGCTGCGATCATGTGTGACAGATTGCCAAGTCAAAATTTGATGTGTTCT 818
QY      221 PheThrHisIleLeu----- 225
Db      819 TTTTACCATATCTTATAGTTTGAATTAATAATATAAGTACACTGAGTGGCACTGTGCT 878
QY      225 ----- 225

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Db      879  CTTGTTCTGGCTTGTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGGAAT  938
Qy      225  -----
Db      939  AAGTCTGTCAATAGTATATGATTAATACTGAGAAATATTACTTCAACATTGACTCAGCAC  998
Qy      225  -----
Db      999  ACCAGATATGCACAACTTGCTTTTGCACTTAATACCTTTTACTTGCTACTGCTTCA  1058
Qy      226  -----
Db      1059  ATGCACAAAAACAGTGAACATCTGCAATTTGACCTGGAACACTTTCCTCAAGCGC  1118
Qy      229  ThGluHISGluLeuLysGlnPheThrGluAspTrpSerGluGluValValSerThrTrp  248
Db      1119  ACAGAAATCATCGCTGAAGCAATTTTACCAAGATTGGTCAGAGAGATGTCTCAACATGG  1178
Qy      249  LeuCyAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetCysAsnIleAspGly  268
Db      1179  CTTTGTGCACAGATTTTAAAGATCTTGCTGTATTTTCAAGATGAATACATTGATGGA  1238
Qy      269  LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu  288
Db      1239  AAAGAACTGTTGAATCTTACAAAGAAAGCTGCTGATGATTTGAAATTTGAATCTCTA  1298
Qy      289  GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu  308
Db      1299  GGACTGCGTACTAAAGTCTGAGAGAAATTTGAAGCTCAGAGCAAGGTTAAATCCCTT  1358
Qy      309  SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro  328
Db      1359  TCTTCAGGAATCTCTGATGATTTTATATGTCCTCAATACAGAACTTATATAAGATCCG  1418
Qy      329  ValIleAlaSerAspGlyIleLysSerGlyLysGluLysGluLysMetGluAsnTrpIleSerLys  348
Db      1419  GTCATCCCATCATGATGCTATTTCATATGAAGAAGCAATGAAATTTGGATCAGCAAA  1478
Qy      349  LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValIleuThrProAsn  368
Db      1479  AAGAAAGCTAACAGTCCCATGACAAATCTTGTTCTTCCCTCAGCGATCTTACCAAAAT  1538
Qy      369  ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys  384
Db      1539  AGGACTCTGAAAAATGCCCATCAATAGATGCGCTGAGACACACCAAAAG  1586

RESULT 13
US-10-077-111-14
; Sequence 14, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Toddlerud, C. Gordon
; APPLICANT: Fanger, Joshua N.
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-4114US2
; CURRENT APPLICATION NUMBER: US/10/077,111
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: RET 16.3 splice variant
US-10-077-111-14
Alignment Scores:
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Pred. No.: 5,1e-222 Length: 1908
Score: 1958.00 Matches: 382
Percent Similarity: 76.29% Conservative: 1
Best Local Similarity: 76.10% Mismatches: 1
Query Match: 95.65% Indels: 118
DB: 14 Gaps: 2
US-10-077-111-13 (1-384) x US-10-077-111-14 (1-1908)
Qy      1  MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAlaCysCysAlaPhe  20
Db      136  ATGTGTAACTGATTCACACATTAGCTGATCATGTGCACATGCAACTGCGCTTTC  195
Qy      21  SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuYrSerLeuArg  40
Db      196  TCTTTTCCCTCTTGCTGCTACTTGTCTTGTGACAAACAAATTTGCCCTGTACTCTTACGT  255
Qy      41  AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyraIaValHisCysCys  60
Db      256  GACTTTACTGAACTGCCACATTTCCATTAAGTTTCATACCTATGCTGTCCACTGCTGC  315
Qy      61  CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu  80
Db      316  TGTTCCTCCCTTCAGACATATTTTGGCATTCGTTCAACAGATGTGACCACTGCTCTA  375
Qy      81  TrpAsnThrGluAsnGlyIleMetLeuAlaValMetGluGlnProSerGlySerProVal  100
Db      376  TGGAAATCTGAATAATGACAGATGCTGCGAGTGTGAACAGCTTATGTGGCAGCCCTGTG  435
Qy      101  ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr  120
Db      436  AGGTTTGCCAGATTTTCCCAAGACTCCACGCTTTGGCATCAGGGCAGCTGATGGAAT  495
Qy      121  ValValLeuTrpAsnAlaGlnSerTyrlLysLeuTyrlArgCysGlySerValLysAspGly  140
Db      496  GTGGTTTGTGATGATGACAGCTCATACAAATATATGATGTGTATGTTAAAGATGCG  555
Qy      141  SerLeuAlaIaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys  160
Db      556  TCTTGGCGGATGTGCATTTTCTCTTAATGAAAGCTTTTGTGACTGGCTCTCATGT  615
Qy      161  GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp  180
Db      616  GGATATTAAACAGTGTGATGAATAAATGAGGTGTCTGATATGTGAAGAACACATGAT  675
Qy      181  LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu  200
Db      676  CTGGAAATTAACCTGCTCCGATTTTCTTCAACAGCAGTTTCTCATGAGAAACAAGGCTT  735
Qy      201  GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer  220
Db      736  CAGTTTTCGACCTGGCATGTGTGTGAGATTTGCCAAGTCAAAATTTGGATGTTTCT  795
Qy      221  PheThrHisIleLeu-----  225
Db      796  TTTTACCATATCTTAGGTTTGAATTAATAATTAAGTACACTGAGTGGGCACTGTGCT  855
Qy      225  -----  225
Db      856  CTTGTTCTGGCTTGTGCTTTTCCCATGANGGCGAGATGCTAGTCAAGGTCAGTGGAAT  915
Qy      225  -----  225
Db      916  AAGTCTGTCAATAGTATATGATTAATACTGAGAAATATTACTTCAACATTGACTCAGCAC  975
Qy      225  -----  225
Db      976  ACCAGATATGCACAACTTGCTTTTGCACTTAATACCTTTTACTTGCTACTGCTTCA  1035
Qy      226  -----AlaArgArg  228
Db      1036  ATGCACAAAAACAGTGAACATCTGCAATTTGACCTGGAACAACCTTTCCAAGCAAGCGC  1095
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QY 229 ThrGluHisGlnLeuYsgInpHeThrGluAspTrpSerGluGluVal1SerThrTrp 248
Db 1096 ACAGAACATCAGCTGAGCAATTTACCGAAGATTGGTCAGAGGAGGATGTCTCAACATGG 1155
QY 249 LeuCyAlaGlnAspLeuYsaAspLeuVal1Gly1LePheLysMetAsnAni1LeAspGly 268
Db 1156 CTTTGTCACAAATTTAAAAGATCTTGTGGTAATTTTCAAGATGAATTAACATTGATGGA 1215
QY 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLys1Le----- 285
Db 1216 AAGAACTGTTGAATCTTACAAAGAAAGTCTGGCTGATGATTTGAAATTTGGCTGGAGT 1275
QY 285 ----- 285
Db 1276 CCTGTGCATGATGATGCTCATGCTGACGCTTCAACCTCTGGGCTCAAGTATCTCTCA 1335
QY 286 -----GluSerLeuGlyLeuArgSerLysValLeuArgLys1LeGluGluLeuArg 302
Db 1336 CCTGGGCTCAATCTCTGAGACTGCGTAGTAAGTGTGAGAAATTTGAAGAGCTCAGG 1395
QY 303 ThrLysValLysSerLeuSerSerGly1LeProAspGluPhe1LeCysPro1LeThrArg 322
Db 1396 ACCAAGCTTAAATCCCTTTCTTCAGGAATTCCTGATGAATTTATATGTCATTAACACTGA 1455
QY 323 GluLeuMetLysAspProVal1Lea1SerAspGly1TySerTyrgLysGluAlaMet 342
Db 1456 GAACCTATGAAGAATCCGATCATGCGATGATGCTATTCATATGAAGAAGCAATG 1515
QY 343 GluAsnTrp1LeSerLysLysLysArgThSerProMetThrAsnLeuVal1LeuProSer 362
Db 1516 GAAATATGGATCGCAAAAGAAAGAAAGTAAAGTCCCAATCTTGTCTTCTTCA 1575
QY 363 AlaValLeuThrProAsnArgThrLeuLysMetAla1LeAsnArgTrpLeuGluThrHis 382
Db 1576 GCGGTACTTACACCAATAGAGACTGTGAATAATGGCCATCAATAGATGCTGAGACACAC 1635
QY 383 GlnLys 384
Db 1636 CAAAG 1641

RESULT 14
US-10-077-111-6
; Sequence 6, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Toddernud, C. Gordon
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-4114US2
; CURRENT APPLICATION NUMBER: US/10/077,111
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: MOUSE
US-10-077-111-6

Alignment Scores:
Pred. No.: 2.55e-181 Length: 1901
Score: 1616.50 Matches: 312
Percent Similarity: 72.06% Conservative: 31
Best Local Similarity: 65.55% Mismatches: 40
Query Match: 78.97% Indels: 93
DB: 14 Gaps: 3

US-10-077-111-13 (1-384) x US-10-077-111-6 (1-1901)

QY 1 MetValLysLeu1LeH1sthrLeuAlaAspHisGly1AspAspVal1AsnCysCysAlaPhe 20
Db 19 ATGTGAGCTGTTGATTTACACAGCTGGCTGATCAGGGAGATGACTCACTGCTGCTTC 78
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThr1LeArg1LeuTySerLeuArg 40
Db 79 TCGGCTGCCCTCTCGGCCACCTGCTCTTGACAAACCATCCGTCTGATCTCCCTTAAGT 138
QY 41 AspPheThrGluLeuProHisSerProLysLysPheHisThrTyrrAlaVal1HisCysCys 60
Db 139 GACTTGTGAACTGCGGTACTCCCGCTGAAGTTTCACACCTATCTGTGCTCACTCTCG 198
QY 61 CysPheSerProSerGly1His1LeuAla1SerCysSerThrAspGly1ThrThrVal1Leu 80
Db 199 TGTTCCTACCCCTCAGAGACACGTTTATGATCGTCTCGACAGACGGAGACAGGTCGTC 258
QY 81 TrpAsnThrGluAsnGly1GlnMetLeuAlaValMetGluGlnProSerGly1SerProVal 100
Db 259 TGGAGCTCGCACCGGACACACCTGACCGGTGTGAGACAGCGGATGACCTCTGTG 318
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAla1SerCysVal1AlaAspGlyThr 120
Db 319 CGGCTGTGCTTCTTCCAGACTCTGCTACCTAGCCGTCAGGGCTGCCGATGATGATCC 378
QY 121 ValValLeuTrpAsnAlaGlnSerTyrgLysLeuTyrgCysGly1SerVal1LysAspGly 140
Db 379 ATGCTTTGTGGATGCACAGACATACAAACTATATAGGTGTGTGTCTGATGATGATGAC 438
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGly1SerPhePheVal1ThrGlySerSerCys 160
Db 439 TCATGTGCTGCTGCTGCTGCTTCTCCGATGAGGCTCTTGTGCTAGCTGCTCTCTGCTG 498
QY 161 GlyAspLeuThrVal1TrpAspArgLysMetArgCysLeuHisSerGly1LysAla1HisAsp 180
Db 499 GGGGACTTGACAGTGTGGAGTGCAGATGAGGTGTCTACACGCGAAGAGGCGACAGAT 558
QY 181 LeuGly1LeThrCysCysAspPheSerSerGlnProVal1SerAspGly1GlnGlnGlyLeu 200
Db 559 CTGGGATGACCGTGCAGAGCTTTCTCTCAGAGCTCTCTCTGGGGAGAA---GGCTTC 615
QY 201 GlnPhePheArgLeuAlaSerCysGly1GlnAspCysGlnVal1Lys1LeTrp1LeVal1Ser 220
Db 616 CAGTCTTACAGATTTGGCGTCATGTGTCAAGACTGTGAATCAAACTTGGCGCTGTACT 675
QY 221 PheThr----- 222
Db 676 ATTAACCGGTCTTAGGCTTTGAATTAATAAAGCACTAAGTGGGCACTGGCCC 735
QY 222 ----- 222
Db 736 CCGTTCGTGGCCGTGCTTTTTCACATGATGGAANAATGCTTGSCATCGGGTCAAGTGAT 795
QY 223 -----His1LeuAlaArgArg 228
Db 796 AAATCTGATCATATAGATGATCGGCCCTCAGAGTGTGTCTACACAGCTGACTCAGCAT 855
QY 229 ThrGluHis----- 231
Db 856 ACCAGGTATGTTAGCACTTGCGGTTTGCACCCAACACTCTTACTTGTCTACTGTTCA 915
QY 231 ----- 231
Db 916 ATGACACAGACAGTGAACATTTGGCAGTTTGACCTGGAACAACCTTCCCAAGCAGGAGAG 975
QY 232 -----GlnLeuLysGlnPheThrGluAspTrpSerGluGluVal1SerThrTrp 248
Db 976 ATGAAACGACCGGTGAACATTTCACTGAAGATGTCTGAGAGAGATGTCTTCCTGTGCTG 1035
QY 249 LeuCyAlaGlnAspLeuYsaAspLeuVal1Gly1LePheLysMetAsnAni1LeAspGly 268
Db 1036 CTTGCTGTCAAAGCTTGAAGACCTGTGCGGATTTTTCAGGGCAACAACATGATGATGG 1095

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Qy 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspLeuLysIleGluSerLeu 288
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Db 1096 AAGAACTATTGCACTTCACAAAGAAAGTGGCTGGTGAATTGAAATCAATCTCTA 1155
289 GlyLeuArgSerLysValLeuArgLysIleGluLeuArgThrLysValLysSerLeu 308
1156 GGGCTGGCGAGCAAAAGCTCGAGAGATTAAGAGCTCAGGGCCAGATGATTCCTC 1215
Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
1216 TCTTCGGAATCCCTGACGAGTTTCATCTGCCCAATACCAAGAACTCATGACAGACCC 1275
Qy 329 ValIleAspAspGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 348
1276 GTCTATCCATCAGATGCTACTCTTACGAGAGAGAGCAATGCAAGCTGATCACAAG 1335
Qy 349 LysLeuArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
1336 AAGAAAGCTACGAGCCCATGCAAAATTTGGCTCTCCCTTCATGTAATGACCCCAAC 1395
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
1396 AGGAACTGAAGAGGCGCATCAACGATGGCTGAGAGCGACGAGAAG 1443
Db

RESULT 15
US-10-956-157-10363
; Sequence 10363, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10363
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-10363

Alignment Scores:
Pred. No.: 2,47e-166 Length: 1400
Score: 1489.00 Matches: 294
Percent Similarity: 75.77% Conservative: 0
Best Local Similarity: 75.77% Mismatches: 2
Query Match: 72.74% Indels: 92
DB: Gaps: 1

US-10-077-111-13 (1-384) x US-10-956-157-10363 (1-1400)
Qy 89 LeuAlaValMetGluGlnProSerGlySerProValArgValCysGlnPheSerProAsp 108
Db 2 CTGGCAGTGAAGAAAGCTTGAAGGAGGCTGAGGAGGTTTCCCGCAGAC 61
Qy 109 SerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValValLeuTrpAsnAlaGlnSer 128
Db 62 TCCACGCTTTGGCATCAGGGGAGCTGATGGAAGTGTGTTTGTGAAGCAGCA 121
Qy 129 TyrIleLysLeuTyrArgCysGlySerValIleAspGlySerLeuAlaAlaCysAlaPheSer 148
Db 122 TACAAATTATATAGATGAGTGTGTTAAAGATGCTCTGGCGGCGCATGCAATTTTCT 181
Qy 149 ProAsnGlySerPhePheValThrGlySerSerCysGlyAspLeuThrValTrpAspAsp 168
Db 182 CCTAATGGAAGCTCTTTGTACAGCTGCTCTCATGTGTGATTTAAACAGTGGGATGAT 241
Qy 169 LysMetArgCysLeuHisSerGlyLysAlaHisAspLeuGlyIleThrCysCysAspPhe 188
Db 242 AAAATGAGGTGTCCGCAATAGTAAAGAACACATGATCTTGGAAATTACCTGCTGGCATTTT 301
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Qy 189 SerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPhePheArgLeuAlaSerCys 208
302 TCTTCACAGCAGATTTCTTGAAGAGAAAGGCTTCAATTTTTCACATGGCAATCATGT 361
Qy 209 GlyGlnAspCysGlnValLysIleTrpIleValSerPheThrHisIleLeu----- 225
362 GGTACAGATTGCCAAGCAAAATTTGATGTTCTTTTACCCATATCTTAAGCTTTTGA 421
Qy 225 ----- 225
Db 422 TTAATAATATAAAGTACACTGAGTGGGCACTGCTCTGTTGCTGTGCTTTTTC 481
Qy 225 ----- 225
Db 482 CATTGAGGAGATGCTAGTCTCAGGGTCAGTGAATAGTCTGTATATATGATTAAT 541
Qy 225 ----- 225
Db 542 AATCTGAGAAATATACCTTACACATTTGACTCAGCACACAGTATGTCACAACTTGCT 601
Qy 225 ----- 225
Db 602 TTGCACTAATAACCTTTTACTTGTCTACTGTTCAATGACAAACAGTAAACATCTGG 661
Qy 226 -----AlaArgArgThrGluHisGlnLysGlnPhe 236
662 CAATTGACCTGCAAAACCTTTGCCAAGAGGCGACAGAAACATCACTGAGCAATTT 721
Qy 237 ThrGluAspTrpSerGluGluValIleSerThrTrpLeuCysAlaGlnAspLeuLysAsp 256
722 ACCGAATATTGGTCAGAGGAGATGTCTCAACATGCTTTGTGCAACAAGATTTAAAGAT 781
Qy 257 LeuValGlyIlePheLysMetAsnAsnIleAspGlyLysGluLeuAsnLeuThrLys 276
782 CTGTGTGATTTTCAAGATGAATATCATGATGGAAGAAAGACTTGAACTTACAAAA 841
Qy 277 GluSerLeuAlaAspLeuLysIleGluSerLeuGlyLeuArgSerLysValLeuArg 296
842 GAAAGTGGCTGATGATTTGAAATTTGAATCTCTAGAGCTGCTGATTAAGTCTGAG 901
Qy 297 LysIleGluLeuLeuArgThrLysValLysSerLeuSerSerGlyIleProAspGluPhe 316
902 AAAATTGAAGAGCTCAGAGCAACAGTTAAATCCCTTCTTCAGGAATTCCTGAGAAATT 961
Qy 317 IleCysProIleThrArgGluLeuMetLysAspProValIleAlaSerAspGlyTyrSer 336
962 ATATGTCCAATTAAGTAAAGAACTTATGAAGATCCGTCATCGCATCAGATGGCTAATCA 1021
Qy 337 TyrGluLysGluAlaMetGluAsnTrpIleSerLysLysArgThrSerProMetThr 356
1022 TATGAAAAAGGAGCAATGGAATTTGATCAGCAAAAAAGAAACGTATCAAGTCCATGACA 1081
Qy 357 AsnLeuValLeuProSerAlaValLeuThrProAsnArgThrLeuLysMetAlaIleAsn 376
1082 AATCTTGTCTTCTTCAAGGGGTACTTACACCAAAATAGACTCTGAAATAGCCATCAT 1141
Qy 377 ArgTrpLeuGluThrHisGlnLys 384
1142 AGATGGCTGGAGACACACAAAAG 1165
Db

Search completed: October 25, 2005, 05:40:07
Job time : 749 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: October 25, 2005, 01:14:43 ; Search time 169 Seconds
(without alignments)
3717.931 Million cell updates/sec

Title: US-10-077-111-13
Perfect score: 2047
Sequence: 1 MVKLITLADHDGVNCCAF.....LTPNRTKMAINRWLETHQK 384

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd
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-USER=US10077111.QCGN_1.1_54.@runat_24102005_072846_8202 -NCPU=6 -ICPU=3
-NO MMAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1978	96.6	1844	4	US-09-620-312D-768
2	234.5	11.5	2359	1	US-08-188-582-4
3	234.5	11.5	2359	1	US-08-646-715-4
4	227	11.1	7028	4	US-09-949-016-4194
5	227	11.1	7028	4	US-09-949-016-4195
6	227	11.1	7042	3	US-09-092-508-1
7	227	11.1	7042	3	US-09-435-115-1
8	227	11.1	7042	3	US-09-098-310-1
9	227	11.1	7042	3	US-09-690-364-21
10	227	11.1	7042	4	US-09-949-016-159
11	227	11.1	7075	3	US-09-092-508-15
12	227	11.1	7075	3	US-09-435-115-15

13	226.5	11.1	2130	4	US-09-620-312D-145	Sequence 145, App
14	220.5	10.8	937	4	US-10-101-464A-251	Sequence 251, App
15	218	10.6	5152	3	US-09-690-364-10	Sequence 10, App
16	217.5	10.6	3747	3	US-09-690-364-17	Sequence 17, App
17	217.5	10.6	7157	4	US-09-949-016-4192	Sequence 4192, App
18	217.5	10.6	7157	4	US-09-949-016-4193	Sequence 4193, App
19	217.5	10.6	7171	4	US-09-949-016-971	Sequence 971, App
20	216	10.6	2152	1	US-08-188-582-17	Sequence 17, App
21	216	10.6	2152	1	US-08-646-715-17	Sequence 17, App
22	203.5	9.9	1246	3	US-09-302-769-22	Sequence 22, App
23	198.5	9.7	2186	3	US-09-184-001-1	Sequence 1, App
24	198.5	9.7	2558	3	US-09-184-001-3	Sequence 3, App
25	195	9.5	7886	2	US-08-751-189-2	Sequence 2, App
26	195	9.5	7886	2	US-09-060-836-2	Sequence 2, App
27	195	9.5	7886	2	US-09-184-445-2	Sequence 2, App
28	193.5	9.5	2369	3	US-09-302-769-20	Sequence 20, App
29	188	9.2	3465	3	US-08-914-999-5	Sequence 5, App
30	187.5	9.2	9991	4	US-09-902-540-1014	Sequence 1014, App
31	187	9.1	1422	4	US-09-248-796A-4567	Sequence 4567, App
32	184.5	9.0	1157	4	US-09-270-767-14727	Sequence 14727, App
33	184.5	9.0	1731	4	US-09-902-540-1920	Sequence 1920, App
34	183.5	9.0	1548	4	US-09-614-221A-136	Sequence 136, App
35	182	8.9	2481	3	US-08-899-578-1	Sequence 1, App
36	180.5	8.8	1698	4	US-09-902-540-8422	Sequence 8422, App
37	180.5	8.8	6553	4	US-09-902-540-885	Sequence 885, App
38	180	8.8	1182	4	US-09-248-796A-4568	Sequence 4568, App
39	178.5	8.7	1542	4	US-09-949-016-1365	Sequence 1365, App
40	176	8.6	1185	4	US-09-248-796A-4600	Sequence 4600, App
41	176	8.6	2272	3	US-09-108-857-1	Sequence 1, App
42	175.5	8.6	1115	1	US-08-190-802A-19	Sequence 19, App
43	175.5	8.6	1115	3	US-08-477-346-19	Sequence 19, App
44	175.5	8.6	1115	3	US-08-473-089-19	Sequence 19, App
45	175.5	8.6	1115	3	US-08-487-072A-19	Sequence 19, App

ALIGNMENTS

RESULT 1
US-09-620-312D-768
Sequence 768, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundang
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_Fl_genes Version 1.0
SEQ ID NO 768
LENGTH: 1844
TYPE: DNA


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: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELE: 910 277299
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2359 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 49..2160
: US-08-188-582-4

Alignment Scores:
Pred. No.: 1,21e-17 Length: 2359
Score: 234.50 Matches: 88
Percent Similarity: 44.34% Conservative: 49
Best Local Similarity: 28.48% Mismatches: 128
Query Match: 11.46% Indels: 45
DB: 1 Gaps: 11

US-10-077-111-13 (1-384) x US-08-188-582-4 (1-2359)

QY 3 Lysleu1le1h1sthr1leu1ala1asp1h1s1gl1y1asp1asp1val1enc1y1cys1ala1phe1ser--- 21
Db 1369 GAGGTAAACCAAGACCTTAATGCTGACACCGGACCCGATACCCCTGTGCTTGCCTTGGCCCC 1428
QY 22 ---PheSer1leu1leu1a1Thr1Cys1Ser1leu1asp1y1Thr1leu1gl1y1Ser1leu1arg 40
Db 1429 GAGATGAACCTGCTCTCTCATGTTCGAGACAGACACCATTAAGCTGTGTCTCTCTC 1488
QY 41 Aspher1hrg1u1eup1ro1h1ser1Pro1eul1y1spher1h1sthr1y1ala1val1h1e1Cys1Cys 60
Db 1489 ACCTGCTCTGCGTA-----GTCACTACCCGCGGACGCTTACCCGCTTGGGATGTT 1542
QY 61 CysPhe1ser1Pro1ser1g1h1s1le1leu1ala1ser1Cys1ser1Thr1asp1y1Thr1Val1leu 80
Db 1543 CGCTTTCGCGCGGACTACTATTGTTCTTCTTCTGTCAGCAAAACTGCTGCTG 1602
QY 81 TTrp1asn1hrg1u1asn1g1y1Met1leu1ala1Val1Met1gl1u1n1Pro1ser1g1y1Ser1Pro1al 100
Db 1603 TGGCCACCGGATTCATCAAGCCGTGCGCTATTCGTGGCTCACTTG---TCCGACGTG 1659
QY 101 Arg1val1Cys1gl1n1Phe1ser1Pro1asp1er1Thr1Cys1leu1ala1ser1g1y1ala1asp1y1Thr 120
Db 1660 GATTGTGTAATTCATCCCAATTCATCAATTAATGTGGCCACGGATTCAGCGATCGCACG 1719
QY 121 Val1Val1leu1Trp1asn1al1ag1n1ser1y1Lys1leu1y1Arg1Cys1g1y1Ser1Val1Lys1asp1y1 140
Db 1720 GTACGCGCTGTGGACACATGACCGGTCACGCGGACGCTGATGACGCGGCACACAGGA 1779
QY 141 Ser1leu1ala1a1Cys1ala1phe1ser1Pro1asn1g1y1Ser1Phe1Phe1Val1Thr1g1y1Ser1Cys 160
Db 1780 TCGGTGAGTTCTTCGGCTCTCTCCGCTGCGCGCGATCTCGGCTCGGGTTCAGTAGAT 1839
QY 161 Gly1Asp1leu1Thr1Val1Trp1Asp1---Asp1y1Met1Arg1Cys1leu1h1ser1Glu1y1Ala1h1s 179
Db 1840 CACAATTCATCACTGTGGATCTGTCCGAACGGATCCCTGGTCAACACCTCTTGAGGCAC 1899
QY 180 Asp1leu1g1y1le1Thr1Cys1Asp1Phe1ser1Ser1gl1n1Pro1Val1ser1asp1y1gl1u1n1g1y 199
Db 1900 ACTAGACACTGTGACACAGATCACCTTAGT-----CCGATGGAAGACGTC-- 1944
QY 200 Leu1gl1n1Phe1Phe1Arg1leu1ala1Ser1Cys1g1y1gl1n1Asp1Cys1gl1n1Val1s1le1Trp1leu1 219
Db 1945 -----CTGGCTGCAGCCGCTTGATTAACAATCACTCTGTG----- 1983
QY 220 Ser1Phe1Thr1h1s1le1leu1ala1Arg1Arg1hrg1u1h1s1gl1n1leu1y1s1gl1n1Phe1Thr1Glu1Asp 239
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Db 1984 -----GACTTGCACAAGCTTACGGAAGAC 2007
QY 240 Trp1Ser1Glu1Val1Val1Ser1Thr1Trp1Leu1Cys1Ala1Gln1Asp1leu1y1Asp1leu1Val1Gly 259
Db 2008 TATATCAGCAATCAATC---ACTGTCTCGACCATCAGATGAGAAGCAGC---GAGGAC 2061
QY 260 Ile1Phe1y1Met1Arg1sn1asn1le1asp1y1y1leu1gl1u-----Leu1leu1Asn1leu1Thr 275
Db 2062 GTCTACTCATGCGGACTTTCCTCCCGACAGAACTCCGCATTGTGTACCTTGCACCTTAC 2121
QY 276 Lys1Glu1Ser1leu1ala1asp1-----Asp1leu1y1s1leu1Ser 287
Db 2122 CGCGAAATCTCTCT-GATGTGCGGTGGGTCTATTCAGAGTTAGAGACAGATTAACCTTA 2180
QY 288 Leu1G1y1leu1Arg1Ser1y1s1Val1leu1Arg 296
Db 2181 TTGTGATACGTATGATGATGTTAAGG 2207

RESULT 3
US-08-646-715-4
: Sequence 4, Application US/08646715
: Patent No. 5637686
: GENERAL INFORMATION:
: APPLICANT: Tjian, Robert
: APPLICANT: Comai, Lucio
: APPLICANT: Dynlacht, Brian D.
: APPLICANT: Hoey, Timothy
: APPLICANT: Ruppert, Siegfried
: APPLICANT: Tanese, Naoko
: APPLICANT: Weinzierl, Robert O.J.
: TITLE OF INVENTION: "TATA-BINDING PROTEIN ASSOCIATED FACTORS,
: TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAIFS AND METHODS OF USE
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,715
: FILING DATE: 09-MAY-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/188,582
: FILING DATE: 28-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELE: 910 277299
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2359 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 49..2160
: US-08-646-715-4
```



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Qy 163 LeuThrValTrrPaAspIysMetArgCysLeuHisSer----- 175
   :::::|||||
Db 3131 ATCAGGCTCTGGAGACAAAGAAAGTATGTAGAAGCTCTGCTGTAATGTAAAGCAGAA 3190
Qy 175 ----- 175
Db 3191 GTAGATGTGTGTTTCAAGAAATGAAGTATGCTTTCAGATTGACCATATNAGAGCT 3250
Qy 176 -----GluYsAlaHisAspLeuGlyIleThr 184
Db 3251 CTGCAACTCATTAATGAGAAAGAGTCAGATTGATTAATCTGACTGAAGCTCAAGTTAGC 3310
Qy 185 CysCysAspPheSerSerGlnProValSerAspGlyGlnGlyIleGlnPhePheArg 204
   |||||
Db 3311 TGCTGTTCCTTAAGTCCACAT-----CTTCAGTAC----- 3340
Qy 205 LeuAlaSerCysGlyGlnAspCysGlnValIysIleTrrPleValSerPheThrHisIle 224
   ::|||
Db 3341 ATTCGATTGTGGAGATGAAGAAATGAGAGCCATGTAGATTGAACCTGTAACATAGAAATC 3400
Qy 225 LeuAlaArgArgThrGlnHisGlnLeuLys-----GlnPheThrGluAspTrr 240
   |||||
Db 3401 TTCAGTCCAGGTTTCAGACACAGAAATCTGTATGCGACATCCAGTTCCAGCCGAT--- 3457
Qy 241 SerGluGluValIaSerThrTrrPheCysAlaGlnAsp-LeuLysAspLeuValGlyIle 260
   :::::|||||
Db 3458 GAGAAAGACTTATTATTCAGT-----TCTGATGATGCTGAATTCAGATTCAGATGAAAT 3508
Qy 260 ePheLysMetAsnHisLeuAspGlyLysGluLeuLysLeuThrLysGluSerLeuAla 280
   |||||
Db 3509 TGGCAATGTGACAAATGTATCTTTCTACAGAGCCATCAGAAACAGTAAAGACTTAA- 3566
Qy 280 AlaAspAspLeuLysIleGluSerLeuGlyLeu-----ArgSerLys 293
   ::|||
Db 3567 -GACTCTTGAAGAAATTCAGAGCTGTTCTGTGATTCATTGATGAGAACAGTAAAGTATGC 3625
Qy 293 sValLeuArgLysIleGluGlnLeuArgThrLysValLysSerLeuSer----- 309
   ::|||
Db 3626 AATATTA-----TTACTGGAATTAAGAAAGACTTGTCTGTCCACAGGATGACATA 3679
Qy 310 -----SerGlyIleProAspGluPheIleCysProIleThrArgG1 323
   ::|||
Db 3680 CTTTCTGTGACATTTCACGATGCTACCA--AGTTTTCATCTACCTGCTGACAGAAAG 3736
Qy 323 uLeuMetLysAspProValIleAlaSer 332
   |||||
Db 3737 ACTGCAAGATCTGAGATTGTGATCTCC 3764

RESULT 5
US-09-949-016-4195
: Sequence 4195, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C0001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4195
: LENGTH: 7028
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-4195

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Alignment Scores:
Pred. No.: 6,636-16 Length: 7028
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: 4 Gaps: 19

US-10-077-111-13 (1-384) x US-09-949-016-4195 (1-7028)
Qy 3 LysLeuLeuHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPheSerPhe 22
   ::|||
Db 2612 GAACTAGACACCTTATGATGATGACACCTCAGACAGACATTCCTGCTCATTTTCCACCAAC 2671
Qy 23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleValGlyLeuTyrSer 38
   |||||
Db 2672 AGTAGATCATGATCTTCTCTTACCCACGCGGCAAGTACGCTTCCTCAAACTTTGGGAT 2731
Qy 39 LeuArgAspPheThrGlnLeuProHisSerProLeuLysPheHisThrTrrValAlaHis 58
   |||||
Db 2732 TTGATACAA-----AAGAAATGCGAAATTCAGTTGCTCATACAAATTCAGTCAAT 2785
Qy 59 CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr 78
   |||||
Db 2786 CACTGCAAGATTTTCCACAGATGATAGACTTTTGGCTAGTTGTTTCCAGCTGATGAAACCTTA 2845
Qy 79 ValLeuTrrPheThrGlnLeuGly-----GlnMetLeu 89
   |||||
Db 2846 AAGCTTGGAGTGGAGATCAGCAAAATGAGAGAAAGCATTAATGTGAAACAGTTCTTC 2905
Qy 90 AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
   ::|||
Db 2906 CTAATTTGAGACCCCTCAAGAGATATGAGATGATGAAAGTTGTTGCTGCTGCT 2965
Qy 107 ProAspSerThrCysLeuAlaSerGlyAlaAlaAspLysThrValIleLeuTrrPAsnAla 126
   |||||
Db 2966 GCTATGATGTCAGAGAAATATGCTG--GACAGCAAAATATAAATCTTTTGTGAAATACA 3022
Qy 127 GlnSer---TrrLysLeuTrrArgCysGlySerValLysAspGlySerLeuAla----- 143
   |||||
Db 3023 GACTCAGCTTCAGAGAGCTGCTGATTCG-----AGAGCAATTAAGTTGGGTT 3070
Qy 144 ---AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp 162
   |||||
Db 3071 CATGCTGATGATTTTCTCTGATGATCATCATTTTTCACATCTTCTGATGACCAACA 3130
Qy 163 LeuThrValTrrPaAspIysMetArgCysLeuHisSer----- 175
   ::|||
Db 3131 ATCAGGCTCTGGAGACAAAGAAAGTATGAAGAACTGCTGTATATGTTAAAGCAGAA 3190
Qy 175 ----- 175
Db 3191 GTAGATGTGTGTTTCAAGAAATGAAGTATGCTTTCAGATTGACCATATNAGAGCT 3250
Qy 176 -----GluYsAlaHisAspLeuGlyIleThr 184
Db 3251 CTGCAACTCATTAATGAGAAAGAGTCAGATTGATTAATCTGACTGAAGCTCAAGTTAGC 3310
Qy 185 CysCysAspPheSerSerGlnProValSerAspGlyGlnGlyIleGlnPhePheArg 204
   |||||
Db 3311 TGCTGTTCCTTAAGTCCACAT-----CTTCAGTAC----- 3340
Qy 205 LeuAlaSerCysGlyGlnAspCysGlnValIysIleTrrPleValSerPheThrHisIle 224
   ::|||
Db 3341 ATTCGATTGTGGAGATGAAGAAATGAGAGCCATGTAGATTGAACCTGTAACATAGAAATC 3400
Qy 225 LeuAlaArgArgThrGlnHisGlnLeuLys-----GlnPheThrGluAspTrr 240
   |||||
Db 3401 TTCAGTCCAGGTTTCAGACACAGAAATCTGTATGCGACATCCAGTTCCAGCCGAT--- 3457
Qy 241 SerGluGluValIaSerThrTrrPheCysAlaGlnAsp-LeuLysAspLeuValGlyIle 260
   ::|||
Db 3458 GAGAAAGACTTATTATTCAGT-----TCTGATGATGCTGAATTCAGATTCAGATGAAAT 3508

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Db 3509 TGGCAATTGACAAATGATCTTTCTACAGCCATCAGAAACGTGAAGACTTTA-- 3566
Qy 280 AASPAAspleuLysIleGluSerLeuGlyLeu-----ArgSerly 293
Db 3567 -GACTCTTGAATAATTCAGACCTCTTCTGTGATTTGATGACAGACGTAGTATGG 3625
Qy 293 sValleuArgLysIleGluGluLeuArgThrLysValLysSerLeuSer----- 309
Db 3526 AATATTA-----TTACTGAAATAAAGAAAAGACTTTGCTGTACACAGGTACACTA 3679
Qy 310 -----SerGlyIleProAspGluPheIleCysProIleThrArgG1 323
Db 3680 CTTTCTGTGACATTTCTCAGCATGCTACCA---AGTTTCATCATCCTGTGACAAAG 3736
Qy 323 uLeuMetLysAspProValIleAlaSer 332
Db 3737 ACTGCAAAAGATCTGAGTTTGATCTCC 3764

RESULT 7
US-09-435-115-1
Sequence 1, Application US/09435115
Patent No. 6346607
GENERAL INFORMATION:
APPLICANT: Henzel, William J.
TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6346607west Center, 90 South seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/435.115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/092.508
FILING DATE:
APPLICATION NUMBER: 60/055.258
FILING DATE: 07-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ketelberger, Ph.D., Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11669.6USU1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7042 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 578...4159
OTHER INFORMATION:
US-09-435-115-1

Alignment Scores:
Pred. No.: 6.65e-16 Length: 7042
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63

Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: 3 Gaps: 19

US-10-077-111-13 (1-384) x US-09-435-115-1 (1-7042)

Qy 3 LysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPheSerPhe 22
Db 2612 GAATTAATACACACCTTATGATGACACTCAGAGCAATCAATTCCTCCATTCACCAAC 2671
Qy 23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTySer 38
Db 2672 AGTAGCATCATCTTCTCTTACCCATGGGTCAAGTCACTGCTTCCCAAACTTGGGAT 2731
Qy 39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyAlaValHis 58
Db 2732 TTGAATCAA-----AAGAATGTCGAATAATCCATGTTGCTCATCAAAATTCGTAAT 2785
Qy 59 CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr 78
Db 2786 CACTGCAGATTTTTCACACAGATGATTAACCTTTGGCTAGTTGTTTCAGCTGATGACCTTA 2845
Qy 79 ValLeuTrpAsnThrGluAsnGly-----GlnMetLeu 89
Db 2846 AAGCTTGGATGCGACATCAGCAAAATGAGAGAAACATTAATGTAAGAACAGTTCTTC 2905
Qy 90 AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
Db 2906 CTAAATTTGAGAGCACCCTCAAGAGATATGAGATGATGATGATGATGATGATGATGAT 2965
Qy 107 ProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValLeuTrpAsnAla 126
Db 2966 GCTATGATGCGAAGATATATGCTG---CGACCAAAATAAATCTTTTGTGTGAATACA 3022
Qy 127 GlnSer---TyrIleLeuTyArgCysGlySerValLysAspGlySerLeuAla----- 143
Db 3023 GACTCAGCTTCAAAAGGCTGATTC-----AGAGACATTTAAGTTGGGTT 3070
Qy 144 ---AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp 162
Db 3071 CAGGTGTGATGTTTCTCGATGATCATCTTTTGACATCTCTGATGACCAAGACA 3130
Qy 163 LeuThrValTrpAspAspLysMetArgCysLeuHisSer----- 175
Db 3131 ATCAGGCTCTGAGACAGAAAGATGTAAGACTCTGCTGTAATTAAGCAAGAA 3190
Qy 175 ----- 175
Db 3191 GTAGATGTGTGTTTCAAGAAATGAAGATGATGCTCTTCACATTCACATATAGACGT 3250
Qy 176 -----GlnLysAlaHisAspLeuGlyIleThr 184
Db 3251 CTGCACACTTATATGAGAAACAGGTCAAGTTGATTTGACTGAAGCTCAAGTTAGC 3310
Qy 185 CysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPheArg 204
Db 3311 TGCTGTGCTTAAGTCCACAT-----CTTCACTAC----- 3340
Qy 205 LeuAlaSerCysGlyGlnAspCysGlnValLysIleThrIleValSerPheThrHisIle 224
Db 3341 ATTGATTTTGGAGATGAATAATGAGCCATGAGATTTTAGAATCTGTAACATAGAAATC 3400
Qy 225 LeuAlaArgArgThrGlnHisGlnLeuLys-----GlnPheThrGluAspTrp 240
Db 3401 TTCAGTCCAGGTTTTCAGCAACAGAAAACGTATGACATTCAGTTCCACGCCGAT-- 3457
Qy 241 SerGluGluValValSerThrTrpLeuCysAlaGlnAsp-LeuLysAspLeuValGlyI1 260
Db 3458 GAGAAAGACTCTTATTTCACT-----TCTCATATGCTGAAATTCAGGTATGGAAT 3508
Qy 260 ePheLysMetAsnAsnIleAspGlyLysGluLeuLeuAsnLeuThrLysGluSerLeuAl 280
Db 3509 TGGCAATTGACAAATGATCTTTCTACAGCCATCAGAAACGTGAAGACTTTA-- 3566

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Qy 280 aaaparpLeuyllegluserleuglyleu-----Argserly 293
Db 3567 -GACTCTGAAATTCAAGACTCTTTCTTGTCATTTGATGCAAGAGTATGCG 3625
Qy 293 vAlleuArgylleglueArgthlyvAllyserleuser----- 309
Db 3626 AATATTA-----TTACTGGAATAAAGAAAAGACTTTGTCTGTCAACGGGTACGTA 3679
Qy 310 -----serglyleproaerpluPhelIecyprolethkrgl 323
Db 3680 CTTTCTTGACATTTCTGACGATGCTACCA---AGTTTCATCTACCTGCTGACCAAG 3736
Qy 323 uLeuMeLyAspProvalIlealaser 332
Db 3737 ACTGCAAGATCTGGAAGTTTGATCTCC 3764

RESULT 8
US-09-098-310-1
; Sequence 1, Application US/09098310
; Patent No. 6403765
; GENERAL INFORMATION:
; APPLICANT: Alimeti, Emed S.
; TITLE OF INVENTION: TRUNCATED APAF-1 AND METHODS OF USE
; FILE REFERENCE: 480140.438
; CURRENT APPLICATION NUMBER: US/09/098.310
; CURRENT FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7042
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (578) ... (4159)
US-09-098-310-1

Alignment Scores:
Pred. No.: 6.65e-16 Length: 7042
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
Gaps: 19
DB: 3

US-10-077-111-13 (1-384) x US-09-098-310-1 (1-7042)
Qy 3 lyeleuileh1sthrleuAlaasph1eglyvAspArValaenCyvSaAlaPheserPhe 22
Db 2612 GACTATATACACACTATGATGACACTCAGACGAATCAATTCCTGCAATTCACCAAC 2671
Qy 23 Ser-----leuAla1aThrCySerleuArlyshrlleatgleytYrSer 38
Db 2672 AGTATGATCATCTCTTCTTATGACACTGGGCTGCAAGTACCTCTTCAAACTTTGGAT 2721
Qy 39 leuAArgArPhethrlyleuArProh1serProleuysRhen1sthrlyAlaValh1s 58
Db 2732 TTGAATGAA-----AAGAAATGTCGAATACCAATGCTTTGGCTCAAAATTCAGTAAT 2785
Qy 59 CyvCyvCyvPheSerProserGlyh1leleuAlaserCyserThraerGlyThrThr 78
Db 2786 CACTGCGCATTTTCAACGATGATAGACTTTTGGCTGATTTGCTTCAAGTATGAACTTA 2845
Qy 79 ValLeuTrpAsnthrGluAenGly-----GlmMetleu 89
Db 2846 AAGCTTTGGGATGGACATCGACAAATGAGAGAAAACATTAAATGAAACAGTTCTTC 2905
Qy 90 AlaValMetGluInProserGlySerPro-----ValArgValCyvGlnPheSer 106
Db 2906 CTAATTTGGAGGACCTTCAGAGAGATATGGAATGATGTAAGTGTGTTCTGAGTCT 2965
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Qy 107 ProAspSerThrCyvleuAlaserGlyAlaAlaAspGlyThrValValLeuTrpAsnAla 126
Db 2966 GCTGATGTCGAAAGATATATGCG---GCAGCAAAATAAATCTTTTGTGAATAC 3022
Qy 127 GlnSer---TyrlleuTyrrArgCyvGlySerVallyleAspGlySerleuAla----- 143
Db 3023 GACTCAGCTTCAAAAGCTGGCTGATTC-----AGAGCAATTTAAAGTTGGCTT 3070
Qy 144 ---AlaCyvAlaPheSerProaenGlyserPheRheValThrclyserCyvGlyuAr 162
Db 3071 CATGCTGATGATTTCTGCTGATGATCATCTTTTTCATCTTTCTGATGACCGAC 3130
Qy 163 LeuThrValTrpArAspArlyswEaArgCyvleuH1ser----- 175
Db 3131 ATCAGGCTCTGGAGACAAAGAAAGATATGTAAGAACTCTGCTATATGTAAGCAAGA 3190
Qy 175 ----- 175
Db 3191 GTAGATGTTGTGTTTCAGAAATGAAGTATGCTGCTTGCAGTTGACCATATAGACGT 3250
Qy 176 -----GluLeuAlaH1leAspRleuGlyl1Thr 184
Db 3251 CTGCAATCTATTATATGAAGACAGCTCAGATTTGATATCTGACGTACAGCTCAAGTTAC 3310
Qy 185 CyvCyvAspPheSerSerGlnProval1serAspGlygluGlnIyGlnInPhrPhaArg 204
Db 3311 TGCTGTGCTTAATGTCACAT-----CTTCAGTAC----- 3340
Qy 205 leuAlaserCyvGlyGlnArCyvGlnVallyG1leTrpIleValserPheThrH1s11o 224
Db 3341 ATTGCAATTGGAGATGAATAATGAGCCATTGAGATTTTGAACCTGTAAACATAGAAC 3400
Qy 225 leuAlaArgArGthrh1h1sglnleuLy-----GlnPheThrGluAspTrp 240
Db 3401 TTCCAGTCCAGCTTATGACCAAGAAACTGTATGACACATCCAGTTCACAGCTCAAT--- 3457
Qy 241 SerGluGluVal1aSerThrTrpleuCyvAlaGlnAsp-LeuLyvAspLeuValGly11 260
Db 3458 GAGAGACTCTTATTTCAAGT-----TCTGATGATGCTGAATTCAGGTATGAAAT 3508
Qy 260 eRheLywMeArAsn1leAspGlyvsglyleuLeuAenleuThlyvGlsu1leuAl 280
Db 3509 TGGCAATTGCAAAATGTATCTTTCTACAGGCCATCAGAAACAGTGAAGCTTTTA-- 3566
Qy 280 aaaparpLeuyllegluserleuglyleu-----Argserly 293
Db 3567 -GACTCTGAAATTCAAGACTCTTTCTTGTCATTTGATGCAAGAGTATGCG 3625
Qy 293 vAlleuArgylleglueArgthlyvAllyserleuser----- 309
Db 3626 AATATTA-----TTACTGGAATAAAGAAAAGACTTTGTCTGTCAACGGGTACGTA 3679
Qy 310 -----serglyleproaerpluPhelIecyprolethkrgl 323
Db 3680 CTTTCTTGACATTTCTGACGATGCTACCA---AGTTTCATCTACCTGCTGACCAAG 3736
Qy 323 uLeuMeLyAspProvalIlealaser 332
Db 3737 ACTGCAAGATCTGGAAGTTTGATCTCC 3764

RESULT 9
US-09-690-364-21
; Sequence 21, Application US/09690364
; Patent No. 6468795
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF APAF-1 EXPRESSION
; FILE REFERENCE: RTS-0190
; CURRENT APPLICATION NUMBER: US/09/690.364
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 21
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1	LENGTH: 7042	
2	TYPE: DNA	
3	ORGANISM: Homo sapiens	
4	FEATURE:	
5	NAME/KEY: CDS	
6	LOCATION: (578) ... (4162)	
7	US-09-690-364-21	
8		
9	Alignment Scores:	
10	Pred. No.:	6.65e-16
11	Score:	227.00
12	Percent Similarity:	40.24%
13	Best Local Similarity:	24.88%
14	Query Match:	11.09%
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Oy 225 LeuAlaArgAlGThrGluHisGlnLeuLys-----GlnPheThrGluLysSrrp 240
Db 3401 TTCCAGTCCAGGTTTCAGCCACAGAAACTGTATGGCATTCCAGTTTCACGCCAT--- 3457
Oy 241 SerGluGluValValSerThr-TripLeuCyAlaGlnAsp-LeuLysAspLeuValGlyI 260
Db 3458 GAGAAAGACTCTTATTTCAGT-----TCTGATGATGCTGAAATTAGGTATGAAT 3508
Oy 260 ePheLysMetAsnAsnIleAspGlyLysGlnLeuLeuAsnLeuThrLysGlnSerLeuAl 280
Db 3509 TGGCAATGAGCAAAATGATGATCTTTCTACAGAGCCATCAGAAACAGTGAACACTTTA-- 3566
Oy 280 AspAspLeuLysIleGlnSerLeuGlyLeu-----ArgSerLys 293
Db 3567 -GACTCTTGAAAAATTCAGACTGCTCTTGTGTGATTCATTTGATGAACACTGAAGGTATGC 3625
Oy 293 sValLeuArgLysIleGlnGluLeuArgThrLysValLysSerLeuSer----- 309
Db 3626 AATATTA-----TTACTGAAAATAAGAAAAGACTTTGTCTGTCCACAGGGTACAGTA 3679
Oy 310 -----SerGlyIleProAspGluPheIleCysProIleThrArgG1 323
Db 3680 CTTTCTTGTCACATTTCTCAGGATCTACCA---AGTTTCATCTACCTCTGTGTGACAAAG 3736
Oy 323 uLeuMetLysAspProValIleAlaSer 332
Db 3737 ACTGCAGAAAGATCTGCAGTTTGTGATCTCC 3764

RESULT 10
US-09-949-016-159
; Sequence 159, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001107
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 7042
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-159

Alignment Scores:
Pred. No.: 6,656-16 Length: 7042
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: Gaps: 19
US-10-077-111-13 (1-384) x US-09-949-016-159 (1-7042)

Oy 3 LysLeuIleHisThrLeuAlaAspHisGlnAspAspValAsnCysGlyAlaPheSerPhe 22
Db 2612 GAACTAGTACACACCTATGATGAGGACCTCAGAGCAAGTCMAATTGTCGCATTTCACCAAC 2671
Oy 23 Ser-----LeuAlaIleThrCysSerLeuAspLysThrIleArgLeuTyrrSer 38
Db 2612 AGTAGTATCATCTTCTTTCAGCCACTGGGTCAAGTACTGCTTCTCAAACTTTGGGAT 2731
Oy 39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrrAlaValHis 58

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Db      2732 TTGAATCA-----AAAGATGTGAAATACCATGTTGTGATACATAAATTCAGTCAAT 2785
QY      59 CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrArgGlyThr 78
Db      2786 CACTGCAGATTTTCAACAGATGATTAACGCTTTGCTAGTTGTTCAAGCTGATGAACTTGA 2845
QY      79 ValLeuThrPenthrgluAengly-----GlnMetLeu 89
Db      2846 AACCTTTGGATGCGACATCAGCAAAATGAGAGAAAACATTAATGCAACGCTTTC 2905
QY      90 AlaValMetGlnGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
Db      2906 CTAATATTGAGAGACCTCAAGAGATATGAGATGATGAGAACTGTTGTTGCTGCTC 2965
QY      107 ProAnpSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValValLeuThrPheAla 126
Db      2966 GCTGATGTGTCAAGATATGCTG--GCAGCAAAAATAAATCTTTTGTGGAAATACA 3022
QY      127 GlnSer---TyrIysLeuTyrArgCysGlySerValLysAspGlySerLeuAla----- 143
Db      3023 GACTCAGCTCAAAAGCTGCGTATGC-----AGAGACATTTTAAGTTGGCT 3070
QY      144 --AlaCysAlaPheSerProAnpGlySerPhePheValThrGlySerSerCysGlyAsp 162
Db      3071 CATGCTGTGATGTTTCTCTGATGATCATCATTTTGAACATCTTCTGATGACACAGA 3130
QY      163 LeuThrValThrPheAspLysMetArgCysLeuHisSer----- 175
Db      3131 ATCAGGCTTGAGAGACAAAGAAAGATGTGAGAACTCTGTAAATGTTAAAGCAAGAA 3190
QY      175 ----- 175
Db      3191 GTAGATGTGTGTTTCAAGAAATGAAGTATGCTCTTGACATGACCATTAAGACGT 3250
QY      176 -----GluLysAlaHisAspLeuGlyIleThr 184
Db      3251 CTCGAACATCATTAATGAGAAACAGGTCAAGTATGATGATGATGAAAGCTCAAGTTAGC 3310
QY      185 CysCysAspPheSerSerGlnProValSerAspGlyGlnGlyLeuGlnPhePheArg 204
Db      3311 TGGTGTGCTTAAGTCCACAT-----CTTCAGTAC----- 3340
QY      205 LeuAlaSerCysGlyGlnAspCysGlnValLysIleThrIleValSerPheThrHisIle 224
Db      3341 ATTGCATTGGAAGTGAATAATGAGCCATTGACATTTTGAACCTGTAAACATAGAAATC 3400
QY      225 LeuAlaArgIleThrGlnHisGlnLeuLys-----GlnPheThrGluAspTrp 240
Db      3401 TTCACATGCCAGGTTTCAGCACAAAGAAACGTATGACACATCCAGTTCACAGCCGAT-- 3457
QY      241 SerGlnGluValLysSerThrTrpLeuCysAlaGlnAsp--LeuLysAspLeuValGlyI 260
Db      3458 GAGAGACATCTTAATTCACAG-----TCGTATATCTGTAAATTCAGGTATGGAAT 3508
QY      260 CpeLysMetAsnAsnIleAspGlyLysGlnLeuLeuAsnLeuThrLysGlnSerLeuAl 280
Db      3509 TGGCAATTGCAAAATGATATCTTCTACAGCCCATCAGAAACAGTGAAGACTTTA-- 3566
QY      280 AspAspLeuLysIleGlnSerLeuGlyLeu-----ArgSerLys 293
Db      3567 -GACTCTTGAATAAATTCAGACATGCTCTTGTGTCATTGTATGAGACAGTGAAGGTATGG 3625
QY      293 eValLeuArgLysIleGlnGluLeuArgThrLysValLysSerLeuSer----- 309
Db      3626 AATATTTA-----TTACTGGAATAAAGAAAAGACTTTGTCTGTCCAGCGGTACAGTA 3679
QY      310 -----SerGlyIleProAspGluPheIleCysProIleThrArgI 323
Db      3680 CTTTCTTGTGACATTTCTCAAGATGACCA--AGTTTCATCTACCTCTGCTGACAG 3736
QY      323 uLeuMetLysAspProValIleAlaSer 332

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Db      3737 ACTGAAAGATCTGAGTTTTGATCTCC 3764
RESULT 11
US-09-092-508-15
; Sequence 15, Application US/09092508
; Patent No. 6291643
; GENERAL INFORMATION:
; APPLICANT: Henzel, William J.
; TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF CASPASE-3
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6291643west Center, 30 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,508
; FILING DATE: 05-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,807
; FILING DATE: 05-JUN-1997
; APPLICATION NUMBER: 60/055,258
; FILING DATE: 07-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kertelberger, Ph.D., Denise M
; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 11669-6USU1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7075 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 578...4192
; OTHER INFORMATION:
US-09-092-508-15
Alignment Scores:
Pred. No.: 6.7e-16 Length: 7075
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: Gaps: 19
US-10-077-111-13 (1-384) x US-09-092-508-15 (1-7075)
QY      3 LysLeuIleHisThrLeuAlaAspHisGlyAspArgValAsnCysCysAlaPheSerPhe 22
Db      2645 GAAGCTAGTACACACCTATGATGACACTCAGACGCAAGTCATTTGCTGCCATTTTACCAAC 2704
QY      23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSer 38
Db      2705 AGTAGCATCATCTTCTCTTACGCACTGGGTCAAGTCAAGTCTGCTCAAACTTTGGGAT 2764
QY      39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHis 58
Db      2765 TTGAATCA-----AAAGATGTGAAATACCATGTTGTGATACATAAATTCAGTCAAT 2818

```


QY 59 CysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr 78
 DB 2819 CACTGCAGATTTTCCACGATGATGAACCTTTGGCTAGTTGTTCACTGATGAACTTGA 2878
 QY 79 ValLeuTrpAsnThrGluAsnGly-----GlnMetLeu 89
 DB 2879 AACCTTGGGATGCAGATCAGCAAAATGAGAAAAACATTAATGCAAACTTCTTC 2938
 QY 90 AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
 DB 2939 CTAAATTGGAGAGACCTCAAGAGATATGAGACTGATGAGAGCTGTGTTCTGTCTCT 2998
 QY 107 ProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValLeuTrpAsnAla 126
 DB 2999 GCTGATGCTGCAGAGATATGCTG--GAGCAAAAAATTAATCTTTGTGGATGACA 3055
 QY 127 GlnSer---TyrLeuLeuTyrArgCysGlySerValLysAspGlySerLeuAla----- 143
 DB 3056 GACTCAGCTTCAAAAGTGGCTGATTC-----AGAGACATTTAAGTTGGGTT 3103
 QY 144 ---AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp 162
 DB 3104 CATGCTGTGATGTTTCTCTGATGATCATCATTTTGCATCTCTGATGACACAGACA 3163
 QY 163 LeuThrValTrpAspAspLysMetArgCysLeuHisSer----- 175
 DB 3164 ATCAGGCTGTGGGACAAAGAAAGTATGTAAGAACTGCTGTAAATGTTAAACCAAGAA 3223
 QY 175 ----- 175
 DB 3224 GTAGATTTGTGTTTCAAGAAATGAGTATGCTCTTGACATTTGACATTAAGACT 3283
 QY 176 -----GluLysAlaHisAspLeuGlyIleThr 184
 DB 3284 CTGCACATCATTAATGAGAAACAGCTCAGATTGATTATCTGACTGAAAGCTCAAGTTAGC 3343
 QY 185 CysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPhePheArg 204
 DB 3344 TGCTGTGCTTAATGTCACAT-----CTTCAGTAC----- 3373
 QY 205 LeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSerPheThrHisIle 224
 DB 3374 ATTCGATTTGGAGATGAAGATGAGCCATTCAGATTTTAAGAACTGTAACAAATGAGATC 3433
 QY 225 LeuAlaArgArgThrGluHisGlnLeuLys-----GlnPheThrGluAspTrp 240
 DB 3434 TTCAGATCCAGGTTTCAGCAACAACTGATGACATCCAGTTCCACAGCCGAT-- 3490
 QY 241 SerGluGluValValSerThrTrpLeuCysAlaGlnAspLeuLysAspLeuValGlyIle 260
 DB 3491 GAGAGACCTCTTAATTCAGT-----TCTGATGATCTGAATTCAGATGATGGAAT 3541
 QY 260 ePheLysMetLysAsnIleAspGlyLysGluLeuLeuAsnLeuThrLysGluSerLeuAla 280
 DB 3542 TGGCAATTGGCAAAATGATATCTTTCTAGAGCCATCAGAAACAGTGAAGACTTTA-- 3599
 QY 280 AlaAspLeuLysIleGluSerLeuGlyLeu-----ArgSerLys 293
 DB 3600 -GACTCTTGAATAAATTCAGACCTCTTCTGTCATTTGATGAGAACATGAGTATGAG 3658
 QY 293 eValLeuAlaGlyLysIleGluGluLeuArgThrLysValLysSerLeuSer----- 309
 DB 3659 AATATTA-----TTACTGGAATTAAGAAAAAGACTTTGTCTCTCAACAGGATACAGTA 3712
 QY 310 -----SerGlyIleProAspGluPheIleCysProIleThrArgI 323
 DB 3713 CTTTCTTGATGACATTTCTGACGATGACCA--AGTTTCATCTACTCTGCTGACAGAG 3769
 QY 323 uLeuMetLysAspProValIleAlaSer 332
 DB 3770 ACTGCAAAAGATCTGAGTTTGTATCTCC 3797

RESULT 12
 US-09-435-115-15
 : Sequence 15 Application US/09435115
 : Patent No. 6346607
 : GENERAL INFORMATION:
 : APPLICANT: Henzel, William J.
 : TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF CASPASE-3
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 : STREET: 3100 No. 6346607 West Center, 90 South Seventh St
 : CITY: Minneapolis
 : STATE: MN
 : COUNTRY: USA
 : ZIP: 55402
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/435,115
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/092,508
 : FILING DATE:
 : APPLICATION NUMBER: 60/055,258
 : FILING DATE: 07-AUG-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Kettelberger, Ph.D., Denise M
 : REGISTRATION NUMBER: 33,924
 : REFERENCE/DOCKET NUMBER: 11669.6USU1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 612-332-5300
 : TELEFAX: 612-332-9081
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 7075 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: Coding Sequence
 : LOCATION: 578...4192
 : OTHER INFORMATION:
 : US-09-435-115-15
 :
 : Alignment Scores:
 : Pred. No.: 6,7e-16 Length: 7075
 : Score: 227.00 Matches: 102
 : Percent Similarity: 40.24% Conservative: 63
 : Best local Similarity: 24.88% Mismatches: 140
 : Query Match: 11.09% Indels: 105
 : Gaps: 19
 :
 : US-10-077-111-13 (1-384) x US-09-435-115-15 (1-7075)
 :
 QY 3 LysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPheSerPhe 22
 DB 2645 GAATCTAGTACACACTTGTATGATGACACCTCAGAGCAAGTCAATTCCTCCATTTCCACCAAC 2704
 QY 23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSer 38
 DB 2705 AGTAGATCATCATCTTCTTAGCCACTGGGCTCAAGTGCATGCTTCCCAAACTTGGCAT 2764
 QY 39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHis 58
 DB 2765 TTGAATCAA-----AAAGAAATGTCGAATAACCATGTTGGTCAATCAAAATTCAGTCAAT 2818
 QY 59 CysCysAspPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr 78

Db	2819	CACCTGCAGATTTTCCACGACGATGATAAGCTTTGGCTTAATTGTTTCAAGCTGATGAACTT	2878
Oy	79	ValLeuTrpAanThrGluAsnGly-----GlnMetLeu	89
Db	2879	AAGCTTTGGGATGCGACATCCAGCAAAATGAGAGAAAACATTAAATGTGMAACAGATTTCTC	2938
Oy	90	AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer	106
Db	2939	CTAAATTGGAGAGACCTTCMAAGAGATATGGAAGTATAGTGAAGTGTGTTGCTGGCTG	2998
Oy	107	ProAapSerThrCysLeuAlaSerGlyValAlaAspGlyThrValValLeuTrpAsnAla	126
Db	2999	GCTGATGTGTCMAAGGATATAGTGTTG--GCAGCAAAAAATAAATCTTTTGTGGAAATCA	3055
Oy	127	GlnSer---TyrLysLeuTyrArgCysGlySerValLysAspGlySerLeuAla-----	143
Db	3056	GACTCAGCTTCMAAGGTGGCTGATTTGC-----AGAGGACATTAAAGTTGGGTT	3103
Oy	144	--AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp	162
Db	3104	CATGGTGTGATGTTTCTTCCTGATGATCATCATTTTGGACATCTTTCGATGACCAGACA	3163
Oy	163	LeuThrValTTPraAspLysPheMetArgCysLeuHisSer-----	175
Db	3164	ATCAGGCTCTGGAGACAAAGAAAGTATGAAGAACTCTGTAATGTTAAAGCAAGA	3223
Oy	175	-----	175
Db	3224	GTAAGTGTGTTGTTTCCAAAGAAATGAAGTATGCTCTTGCAATTTGACATATAAGACGT	3283
Oy	176	-----GluYsAlaHisAspLeuGlyTLeThr	184
Db	3284	CTGCAACTCATTAATGAGAAGAAACAGGTCCAGATTGATTTCTGACTGAAGCTCAAGTTAGC	3343
Oy	185	CysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeuGlnPhePheArg	204
Db	3344	TGCTGTGCTTAAAGTCCACAT-----CTTCAAGTAC-----	3373
Oy	205	LeuAlaSerCysGlyGlnAspCysGlnValLysIleTyrIleValSerPheThrHisIle	224
Db	3374	ATTGATATTGGAGATGAATAATGAGACCATTTAGATTTTGAAGAACTGTAAACAATAGATC	3433
Oy	225	LeuAlaIArgThrGlnHisGlnLeuLys-----GlnPheThrGlnAspTTrp	240
Db	3434	TTCCAGTCCAGGTTTCACACACAGAAACTGTATGGCAATCCAGTTCACGCCGAT--	3490
Oy	241	SerGlnGluValAlaIserThrTyrPheCysAlaGlnAsp-LeuLysAspLeuValGlyIle	260
Db	3491	GAGAAAGACTCTTATTTCAAGT-----TCTATGTAGTCTGAATTCACAGTATGGAT	3541
Oy	260	ePheLysMetAsnAsnIleAspGlyLysGlnLeuLeuAsnLeuThrLysGlnSerLeuAl	280
Db	3542	TGGCAATTGACAAATGATGATCTTTCTACGAGGCCATCAGAAACAGTGAAGACTTA--	3599
Oy	280	AspAspLeuLysIleGlnSerLeuGlyLeu-----ArgSerLys	293
Db	3600	-GACTCTGAAAAAATTCAGAACTGCTTTCTTGTCATTTGATGAAACAGTGAAGTATGG	3658
Oy	293	sValLeuArgLysIleGlnGluLeuArgThrLysValLysSerLeuSer-----	309
Db	3659	AATATTA-----TTACGGAATAATGAAGAAAGCTTTGCTGTCACACAGGTAACGTA	3712
Oy	310	-----SerGlyIleProAspLeuPheIleCysProIleMetArgGly	323
Db	3713	CTTCTCTTGATGACATTTCTCAGCATGCTTCA--AGTTTCATCTAACCTGCTGACAAAG	3769
Oy	323	uLeuMetLysAspProValIleAlaSer	332
Db	3770	ACTGCAAGATCTGGAGTTTGTGATCTCC	3797

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; Sequence 145 Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhimei
; APPLICANT: John Thilingshast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662ol Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_genes Version 1.0
; SEQ ID NO 145
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (184)..(1236)
; US-09-620-312D-145
Alignment Scores:
Pred. No.: 9, 6e-17 Length: 2130
Score: 226.50 Matches: 96
Percent Similarity: 41.05 Conservative: 60
Best Local Similarity: 25.26 Mismatches: 137
Query Match: 11,068 Indels: 88
DB: 4 Gaps: 15
US-10-077-111-13 (1-384) x US-09-620-312D-145 (1-2130)
QY 25 LeuAl1ThCySer1euaSpr1yThr1leArg1euTySer1euaYgAnrPhnTh1Glu 44
Db 149 CTAGCTACAGCTTCGTGAGACAAATCCATAATGATGAGAGCATG-----TATCGCAG 202
QY 45 LeuPnH1SerP1eUe1yShn1e1Th1rYAla1Aln1CyScyScySPn1SerP1 64
Db 203 CGCTTCCTGATATTCCTGGATGACATACACACTGTGATCCCTGTGCCA-ATTGTAACC 261
QY 65 SerG1yAl1e1leuAl1a1SerCySerTh1n1SprG1yTh1rYAl1eU1rP1n1Th1G1u 84
Db 262 GATGGAAGACATAATGTTGTGTCATGTAGTAGGATTAACCTTAATAATTGGATACACA 321
QY 85 AsnG1yG1m1e1leuAl1a1Val1Me1c1u1n1r1o1SerG1y1SerP1roV1a1nG1yG1n 104
Db 322 AATTAACCAATGCTTAATTAATCTTCAGATTCCTGTTGATTT---GCAATTTTGTGAC 378
QY 105 Ph1SerP1roA1SerTh1rCy1eua1a1SerG1yAl1a1Ala1SprG1yTh1rYAl1eU1rP 124
Db 379 TTTAACCTTAAGTGATACATGATACCTTCACAGAGTTCTGATCAAACTGTGAAGTCTCG 438
QY 125 AsnAl1G1n1SerTy1rY1leU1rY1rG1Cy1Sc1y1SerYAl1y1eA1SprG1y1Ser1eUAl1a1 144
Db 439 GATGTAAGGTGAACAATTAATTAATCAATTAACCAAGTATCAACGGGTGGAGTTAATTGC 498

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Db 716 GGGCCCCCATTTTACCTGTGCCCCCATCTTCAGAGAAATATGATGATCTCCAGATTGCG 775
QY 332 SerAspGlyTyrSerTyrGlyIleuAlaMetGluAsnTrpIleSerLysLysArg 351
Db 776 GCGGATGGTTCTTCACTTATGAGAGAAAGCTATATGCGGAATGGTTGGACAAACGACCATGAT 835
QY 352 ThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsnArgThrLeu 371
Db 836 ACATCCCAATGACCAACTGGAAGCTTAGTCATTGGATCTCACTCCCAACCAACGCGCTTA 895
QY 372 LysMetAlaIleAsnArgTrpLeu 379
Db 896 CGGTGGCAATTCAGAGTGGCTC 919
RESULT 15
US-09-690-364-10
; Sequence 10. Application US/09690364
; Patent No. 6468795
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Walc
; TITLE OF INVENTION: ANTISENSE MODULATION OF APAF-1 EXPRESSION
; FILE REFERENCE: RTS-0190
; CURRENT APPLICATION NUMBER: US/09/690.364
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 10
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (586) ... (4302)
US-09-690-364-10

Alignment Scores:
Pred. No.: 4.83e-15 Length: 5152
Score: 218.00 Matches: 65
Percent Similarity: 39.15% Conservative: 27
Best Local Similarity: 27.66% Mismatches: 75
Query Match: 10.65% Indels: 68
DB: 3 Gaps: 6

US-10-077-111-13 (1-384) x US-09-690-364-10 (1-5152)

QY 3 LysLeuIleIsthrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPheSerPhe 22
Db 2620 AACCTTGTGACACCTTAACGACGACACTCGAGCAAGTCAATGGCTGCCATTTCACCAAC 2679
QY 23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSer 38
Db 2680 AGTAGTAACCACTCTCTGGCCACCGGGTCAATGATTTCTTCCTCAAGCTCTGGGAT 2739
QY 39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHis 58
Db 2740 TTGAATCAA-----AAAGAAATGCGAAATACCATGTTGGTGCACACGAACTCAGTCAC 2793
QY 59 CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr 78
Db 2794 CACTGACAGTTCTTCACCAAGACGATGAGCTTTGGCTAGCTGCTCAGCTGACGGGACTTTA 2853
QY 79 ValLeuTyrAsnThrGluAsnGlyGln----- 87
Db 2854 AGGCTTTGGATGTGAGATCAGCAAAACGAGAAAGCATTAATGTAAGCGCTTCTTC 2913
QY 87 ----- 87
Db 2914 CTGAGTTCAAGAGACCTCCAGAGATGAGAGTATCGTGAAGTGTGTTCTGTGTC 2973
QY 87 ----- 87
Db 2974 GCAGATGTGACAAATAATATAGTGGACGAAAAAACAAGTCCCTTTTGTGATATTCAT 3033

QY 88 -----MetLeuAlaValMetGluGlnProSerGlySerProValArgValCysGln 104
Db 3034 ACTAGTGGCCTATTGGCAGAGATCCACACAGGCCATCACAGCAATCCAGTACTGTGC 3093
QY 105 PheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValLeuTrp 124
Db 3094 TTCTCCCTCATGACCATTTGGCTGTGATGGCCCTGTCTCAGTACTGTGTGGATTTGTGG 3153
QY 125 AsnAlaGlnSer---TyrLysLeuTyrArgCysGlySerValLysAsnGlySerLeuAla 143
Db 3154 AACATAGACTCCCGCCTMAAGTGGCCGACTGC-----AGAGACATTGAGT 3201
QY 144 -----AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db 3202 TGGCTTCACGGTGTGATGTTTCTCCGATGGCTCTCATTTTGTGACAGCTTGTGATGAC 3261
QY 161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSer 175
Db 3262 CAACAATAGAGGTCTGGGAGACAAAAAGTATGCAAGAACTCT 3306

Search completed: October 25, 2005, 04:10:59
Job time : 209 secs